Thesis/
Reports
Strickland
D.

Small Mammal Faunas in Aspen and Conifer Forests : The Effects of Macro- and Microhabitat Variation

Final report RM-4201.1-2

SMALL MAMMAL FAUNAS IN ASPEN AND CONIFER FORESTS: THE EFFECTS OF MACRO- AND MICROHABITAT VARIATION

Final Report RM-4201.1-2
May 31, 1992

DALE STRICKLAND
Principal Investigator
Department of Statistics
University of Wyoming

JANE SHRIVER
Graduate Student
Department of Statistics
University of Wyoming

DEBORAH FINCH
Forest Service Departmental Representative
Rocky Mountain Forest and Range Experiment Station

LIBRARY COPY
ROCKY MTN. FOREST & RANGE
EXPERIMENT STATION

List of Tables iii

List of Figures iv

INTRODUCTION 1

METHODS 3
Data collection 3
Estimation of mammal densities 6
Vegetation variables 12
Repeated measures analysis 13
Logistic regression 14

RESULTS 16
Mammal densities 16
Repeated measures analysis 17
Habitat selection functions 18

DISCUSSION 19

LITERATURE CITED 21

APPENDICES
APPENDIX A. Trapping data A.1
APPENDIX B. Vegetation
APPENDIX B.1. Sampling protocol B.1
APPENDIX B.2. Computations for summary variables . B.2
APPENDIX C. Chi-square test C.1
APPENDIX D. Minimum sufficient statistics D.1
APPENDIX E. Boundary strip estimates E.1
APPENDIX F. Repeated measures analysis F.1
APPENDIX G. Habitat selection functions G.1
APPENDIX H. Variable selection steps for *Clethrionomys gapperi* H.1

List of Tables

Table 1. Return rates for six small mammal species captured in the central Rocky Mountains in 1987-1989. 26

Table 2. Probabilities for first capture and recapture for six small mammal species captured in the central Rocky Mountains in 1987-1989. 26

Tables 3-4. Mean abundance of small mammals for each habitat, region and year. 27

Tables 5-6. Mean densities estimates of small mammals for each habitat, region and year. 29

Tables 7-18. Vegetation variables averaged within each habitat region and year. 31

Table 19. RMANOVA for Clethrionomys gapperi. 41

Table 20. Least square means for Clethrionomys gapperi 42

Table 23. HSF's for Clethrionomys gapperi. 45

Table A.1. Frequency count for all mammals trapped. A.1

Table C.1. Chi-square tests C.1

Table D.1 Minimum sufficient statistics D.1

Table E.1 Boundary strip estimates E.1

Table F.1 RMANOVA for Microtus montanus F.1

Table F.2 Least square means for Microtus montanus F.4

Table F.3 RMANOVA for Peromyscus maniculatis F.5

Table F.4 Least square means for Peromyscus maniculatis F.6

Table F.5 RMANOVA for Sorex cinereus F.9

Table F.6 Least square means for Sorex cinereus F.10

Table F.7 RMANOVA for Sorex monticolus F.13

Table F.8 Least square means for Sorex monticolus F.14

Table F.9 RMANOVA for Tamias minimus F.17

Table F.10	Least square means for *Tamias minimus*	F.18
Table F.11	RMANOVA for *Zapus princeps*	F.21
Table F.12	Least square means for *Zapus princeps*	F.22
Table F.13	RMANOVA for *Microtus longicaudus*	F.25
Table F.14	Least square means for *Microtus longicaudus*	F.26
Table G.1	Coding for design variables	G.1
Table G.2	Variables removed with VIF procedure	G.1
Tables G.3-G.22	HSF's for six small mammal species	G.2
Tables H.1-H.6.	Variable selection steps in Logistic regression	H.1

List of Figures

Fig. 1. Graphs of LS means for Clethrionomys gapperi 45

Fig. 2. Graphs of LS means for Microtus montanus F.3

Fig. 3. Graphs of LS means for Peromyscus maniculatis F.7

Fig. 4. Graphs of LS means for Sorex cinereus F.11

Fig. 5. Graphs of LS means for Sorex monticolus F.15

Fig. 6. Graphs of LS means for Tamius minimus F.19

Fig. 7. Graphs of LS means for Zapus princeps F.23

Fig. 8. Graphs of LS means for Microtus longicauduas F.27

INTRODUCTION

Quaking aspen (Populus tremuloides) is the dominant tree species in over 2 million hectares of montane and subalpine forests in the central Rocky Mountains (DeByle 1985). About 75% of aspen stands in the central Rockies are mature and over mature and clearcut logging has been suggested as a regenerative procedure to induce vegetative sprouting. The increased demand for aspen products and concern over a lack of stand regeneration has created an interest in determining its multiple use values.

Because aspen forests occur over a wide latitudinal gradient in the Rocky Mountains, the study was designed to identify variation in mammalian species composition in aspen forests occupying two different latitudes. Because mature aspen forests are targeted for lumbering, the focus of this study is the fauna in mature aspen, aspen-conifer, and conifer stands. Critical questions are 1) what mammals occur only in aspen habitats or conifer habitats, 2) what species reach peak abundance in aspen but occur in conifer habitats as well, 3) which species prefer mixed aspen-conifer habitats over aspen or conifer.

Various models exist for estimating densities with capture-recapture data. These models were assessed and a new method for estimating abundances was developed by estimating the probability of capturing an animal at least once, P, from pooled data and the Lincoln-Peterson estimator. This technique was developed from discussion in George Menkins and Stan Anderson's paper in 1983 and designed to compensate for small samples of capture-recapture

data on individual trapping grids. The model built in program CAPTURE (White et al. 1991) that allows probability to vary with behavioral response and individual heterogeneity, M_{bh}, was also used to estimate P.

Trapping tendencies for individual species determined which method was used for estimating abundances. The M_{bh} model in program CAPTURE was used if a species displayed trap happiness or trap shyness, otherwise P was estimated with the Lincoln-Peterson model. Trapping tendencies were determined from a ratio between the number of recaptures and the number of opportunities to be recaptured and the capture probabilities in the Zippin model in program CAPTURE (Otis et al. 1978).

Abundance estimators were computed for eight small mammal species in three forest types over two regions. Comparisons of abundances between forest types, regions and years were evaluated in a repeated measures analysis where year was the repeated measure. Relationships between vegetation features and the presence or absence of small mammals were also evaluated in habitat selection functions built in logisitic regression.

METHODS

Data collection

Small mammal trapping and sampling of vegetation occurred from 1987 through 1989. Sampling occurred in two geographically distant areas identified as north and south regions. The north region was located in the Medicine Bow National Forest and the Routt National forests of southern Wyoming and northern Colorado.

The south region occurred in parts of the Grand Mesa, Uncompahgre and Gunnison National forests in south central Colorado.

Fifteen plots were established within each region. Nine plots were approximately 90% quaking aspen (Populus tremuloides), three were approximately 90% Engelmann spruce (Picea englemannii) and subalpine fir (Abies lasiocarpa), and three had an approximate 50:50 ratio of aspen and Engelmann spruce/subalpine fir. All plots were at least 40 hectares in size and ranged from 2300 m to 2700 m in elevation.

A 150 X 180 meter trapping grid was established on 30 plots in 1987. However, because of dense vegetation the dimension of the grids was reduced in the south region to 150 X 150 meters in 1988 and 1989. The trapping grids remained 150 X 180 in the north region through 1988 and 1989. The grid configurations were 10 rows by 10 columns in the south and 10 rows by 12 columns in the north. Sherman live traps (7.6 cm X 8.9 cm X 23 cm) were set at each grid point 15 meters apart (100 on the 10 X 10 plots and 120 on the 10 X 12 plots). Pitfalls were located at every other trapping point (25 on the 10 X 10 plots and 30 on the 10 X 12 plots). Commercial rolled oats and rat pellets were the main bait (Finch and Reynolds 1988).

Each plot had exactly one sampling period per year in August and September. In 1987 there were eight trap nights per sample period and the traps were checked once a day. In 1988 and 1989 the number of trap nights was reduced to six. Toe clipping was used to uniquely mark each animal captured. Data on sex,

reproductive conditions, weight and length were recorded on field sheets and later entered in an electronic data file. Mortalities were tagged and preserved in an alcohol solution. At a later date they were examined in a lab and data were recorded on specimen reports. Data on mortalities were also entered in the electronic data file and replaced field data if there were identity or measurement discrepancies.

Field crews in the north and south regions used two different sampling procedures for collection of vegetation data. The crew in the north region collected data on a random sample of trap-sites on each plot each year. However, the collection procedures in the southern region deviated somewhat from this format and could not be considered a true random sample of the vegetation in each plot. We decided if the data were well distributed spatially the plog could be described with the data collected. Therefore, a Chi-square goodness of fit test was performed to test for spatial coverage of the sample points. Vegetation sample points for each plot in the south were pooled over years and trapping points were grouped into nine cells. Chi-square goodness of fit tests with eight degrees of freedom were run to test for equal cell frequency of sampling points. Given that the chi-square tests (appendix C, table C.1) were not significant data were assumed to consist of a systematic sample from each plot.

Vegetation measurements were taken all three years in the north region but crews in the south region recorded vegetation

measurements in 1988 and 1989 only. The sampling protocol can be found in appendix B.1.

The mammal count data and the vegetation data were edited for data entry errors and both data sets were sampled to check for data integrity. The formats for both data sets were restructured to facilitate analysis. The formats for both data sets were restructured to facilitate analysis. There are two format for the mammal count data. The first format consists of one record for each trap night an animal was trapped and are found in three files according to year, TRAP87.DAT, TRAP88.DAT, and TRAP89.DAT. These data were restructured so that one record included the total trapping history for each animal. These data are stored in three files according to year called T87.DAT, T88.DAT, and T89.DAT. Vegetation data were entered into three files according to year and one record wass thirteen lines long. There were three line formats for each record. Three new files were bult according to these line formats and are called VEG1.DAT, VEG23.DAT, and VEG4.DAT.

Estimation of Mammal Densities

The number of animals present in each plot and corresponding density estimates were needed for data analysis. The parameters estimated included population size and capture or recapture probabilities (White et al. 1982). Pollock (1991) reviewed several models that estimate these parameters.

In this study we assumed that populations were closed when making estimates. However, the assumption of equal probability

of capture did not hold for all species. Various models have been constructed that allow for varying probabilities of capture (Otis et al. 1978). These models are composed of probabilities of capture that vary with time or trapping occasion, species behavioral responses, characteristics of individual animals, and combinations of these variables. We chose the simplest model that "fit" the data providing the model had a theoretically appropriate estimator.

Menkins and Anderson (1988) found that the Lincoln-Peterson estimator (Seber 1982) worked just as well as any other estimator except when the animals displayed trap happiness or trap shyness. The M_{bh} model in program CAPTURE (White et al. 1991) allows for the probability of capture to change according to individual heterogeneity as well as behavioral response (Otis et al. 1978). Therefore, abundance estimates for those species that tended to be trap happy or trap shy were found using capture probabilities in the M_{bh} model, and those that did not indicate this tendency were estimated using a form of the Lincoln-Peterson estimator. Estimates from these models were found as follows.

Two measures were used to determine the trapping tendencies for each species. The first was found by calculating a return rate for each trapping occasion. This index was computed in fortran language (HS1.FOR) by summing the number of opportunities for recapture after a given trapping night and dividing it into the sum of actual recaptures after that same night. We assumed this ratio indicated trap happiness if it increased over the

trapping period. We used the probability of a first capture (p-hat) and the probability of recapture (c-hat) from the Zippin model (Otis et al. 1978) in program CAPTURE (White et al 1991) using the XY-complete matrix as the second measure of trapping tendencies. From this model we assumed trap happiness was indicated if c-hat was larger than p-hat. In both cases the animals that died in the traps were removed because they did not have an opportunity to be recaptured.

Two species, Sorex cinereus and Sorex monticolus, were considered special cases. These species had a high death rate in the traps and had very few recaptures. As a result it was impossible to estimate their return rates or recapture probabilities. These species were assumed to be removed from the population as required by the M_{bh} model and thus abundance was estimated using this model.

To compensate for small number of captures, data were pooled across years (3 years) and plots (30 plots) for each species and each habitat to obtain the mean probability of capturing a unique animal at least once within a given habitat type, P=Pr(C). We then divided this probability into the number of total unique animals caught in a particular grid during a particular year, M (90 population estimates). These data were placed in the following format.

$$
\begin{array}{llll}
X_{1111} & X_{1112} & \cdots & X_{11n_a} \\
X_{1121} & X_{1122} & \cdots & X_{112n} \\
\vdots & \vdots & & \vdots \\
\vdots & \vdots & & \vdots \\
\vdots & \vdots & & \vdots
\end{array}
$$

$$
\begin{array}{llll}
X_{11m1} & X_{11m2} & \cdots & X_{11mn} \\
X_{1211} & X_{1212} & \cdots & X_{121n} \\
X_{1221} & X_{1222} & \cdots & X_{122n} \\
\vdots & \vdots & & \vdots \\
X_{12m1} & X_{12m2} & \cdots & X_{12mn} \\
\vdots & \vdots & & \vdots \\
X_{1km1} & X_{1km2} & \cdots & X_{1kmn} \\
\vdots & \vdots & & \vdots \\
X_{skm1} & X_{skm2} & \cdots & X_{skmn}
\end{array}
$$

where s=number of years.
k=number of plots
m=number of animals
n=number of trapping nights.

The unbiased Lincoln-Peterson estimate (Seber 1982), N^{*}_{ij}, was found by collapsing the first three trapping nights for n_1=number of "marked" individuals and the last three trapping nights for n_2=number of recaptures (Menkins and Anderson 1988) for i^{th} plot of j^{th} year. These estimates were then transformed into probabilities to obtain the overall P by dividing the total number of different animals caught less the total that died in the first period, d_{ij}, by the sum of N^{*}_{ij};

$$P=\frac{\sum\sum (M_{ij}-d_{ij})}{\sum\sum N^{*}_{ij}} \qquad (1)$$

The population estimate on one plot for one year is then found by dividing

$$N_{ij}=M_{ij}/P \qquad (2)$$

(McDonald, personal communication). The dead animals were subtracted from the total count in the first period because they

did not have the opportunity to be recaptured in the second period and N^{*}_{ij} is an estimate of the population size at the time of release of marked animals. If within a given plot $n_1=0$, $n_2=0$, or $m_2=0$ (ie recaptures) then the respective plot did not contribute to the probability estimator. A fortran program called LP1.DAT was built to compute these estimators.

The input for program CAPTURE (White et al. 1991) can be of two forms, the capture history matrix or minimum sufficient statistics. Problems arose with the capture history matrix because some marked animals died. Their probability of recapture could not be computed because they did not have an opportunity to be recaptured. However, the population present during the trapping periods would not be represented if these animals were removed from the capture history matrix. The minimum sufficient statistics for the M_{bh} model are the total number of unmarked animals captured on the j^{th} night, $u_j=n_j-m_j$, and are not dependent on the survival rate. For this reason these statistics (appendix D, table D.1) were used as input for the M_{bh} model in program CAPTURE (the command file was called ZIPEST.DAT).

When using the M_{bh} model CAPTURE computes an average conditional probability of capture on the j^{th} occasion for those animals not previously captured, p_j, $j=1,2,\ldots,k,\ldots,t$ (Otis et al, 1978). CAPTURE then assumes that $p_k=p_{k+1}=\ldots=p_t$ and $p_1,\ldots,p_{k-1}$ are not equal, and computes an associated Chi-square goodness of fit test. Two estimators are listed on the printout provided by CAPTURE. The first is the estimator associated with the smallest

k that fits the data according to the goodness of fit test. The second estimator is from Pollock and Otto (1983) and tends to have better precision than the first. Therefore we selected the average conditional probabilities of first capture associated with the estimator closest to the Pollock and Otto estimator without a significant Chi-square. These probabilities were then used to find the probability of capturing an animal at least once

$$P=1-[(1-p_1)(1-p_2)\ldots(1-p_6)]. \quad (3)$$

The population abundance estimate on the i^{th} plot, j^{th} year was

$$N_{ij}=M_{ij}/P, \quad (4)$$

where M_{ij} is the number of different animals caught on the i_{th} plot, j_{th} year.

Abundance estimators were used when one species was considered at a time in an analysis. Density estimates, estimates of the number of animals per unit area trapped, were used in analyses that considers more than one species at a time. An estimate of the effective area trapped on a grid was needed because it may not be the same size as the actual grid. One half of the average maximum distance between points where an animal was trapped (Cottam 1953) was computed and used to estimate a boundary strip for each species in each habitat type (appendix C). Density was estimated by dividing the abundance estimator by the sum of the area of the boundary strip and the area of the grid,

$$D = \frac{\text{abundance}}{\text{(area grid + area boundary strip)}} . \quad (5)$$

A fortran program called DENSITY.FOR was written to compute these estimates.

Several species captured did not have an adequate number of captures and recaptures to estimate abundance whether the data were pooled or not. Thus, a catch per unit effort index was found for each species

$$CPUE = \frac{\text{number animals caught}}{\text{(number of possible traps)(number of trapping nights)}} . \quad (6)$$

The number of trap nights per sample session was inconsistent over the three years. Therefore, the seventh and eighth trap nights from the first year were dropped from the data set.

Vegetation variables

Most of the raw vegetation data were not in a suitable format for analysis and required transformation. Density of trees for each plot was estimated using the point-centered-quarter-circle sampling method (Pollard 1971). Percent shrub was estimated using line-intercept theory. Horizontal cover measurements (see appendix B.1 #4) for herbs and shrubs were converted into means. Means for tree diameters and distances from the center of sample points were computed and a ratio of the mean diameter and mean distance was found. A categorical variable indicating the type of trees present at a point was constructed. Also a density estimate of the logs and trees was

found by dividing the size of the area searched into the number of trees/logs present at each point. These computations were executed in SAS packages (SAS 1989). The command files are called SUM1.SAS, SUM23.SAS, and SUM4.SAS, and the input files are VEG1.DAT, VEG23.DAT, and VEG4.DAT, respectively.

Repeated measures analysis

Repeated measures analysis was performed in SAS packages (The command file is RMABUN.SAS) using the abundance estimators for each plot in each year as the response variable, the type of habitat and regional area as the grouping variables, and year as the repeated measure (the SAS command file is RMABUN.SAS). The model to describe the abundance level with these parameters is

$$Y_{ijkl} = \mu + R_i + H_j + RH_{ij} + P_{(ij)k} + T_l + RT_{il} + HT_{jl} + RHT_{ijL} + PT_{(ij)kl} \quad (7)$$

where R=region, H=habitat, T=year, and P=plot. There are two levels of experimental units, plots and years, therefore there are two error terms in the model, $P_{ij(k)}$ and $PT_{(ij)kl}$. All terms are fixed effects and plots are nested within region and habitat.

Compound symmetry or equal variances and covariances are necessary for valid F-tests in repeated measures analysis of variance tables (Milliken and Johnson 1984). The Huynh-Feltd condition, which is a generalization of compound symmetry, was used to validate F-tests. This condition specifies that differences between each pair of error terms are equal. A measure was developed by Box (1954) that tests whether or not the

Huynh-Feltd condition is satisfied. If this condition is not satisfied an adjustment in the F-test is constructed using unbiased estimators for the numerator degrees of freedom and the denominator degrees of freedom from Box's epsilon. This adjusted F-test was the test used to determine significant differences in the main effects and interactions in the model.

Logistic regression

Logistic regression was used to build habitat selection functions for each species. These models were then used to estimate the probability of use at each point. The vegetation summary variables were used as the predictor variables in the models.

There were 26 vegetation variables describing ground cover, shrub cover and tree cover at each sample point on each plot. Correlation among these variables was tested for using the variance inflation factor (VIF) in PROC REG of SAS packages. If correlation exists among variables this index will measure the inflation in variances for parameter estimates in a multiple regression model. A variable is highly correlated with at least two other variables when the VIF is high. Therefore, the variable with the highest VIF was removed from the model. If two or more VIF's were similar we decided to remove the variable that was more difficult to measure or estimate, or remove the variable that was considered the least important biologically. This process was repeated using the reduced models until the variance inflation factors were all within the range of 2.

Three categorical variables (stem type, grass or sedge dominance, and soil type) were coded into dummy variables for the logistic regression procedure. These variables are tabled in appendix E.

Binary variables indicating whether a particular animal was trapped (USE=1) or not trapped (USE=0) at each point with vegetation were constructed. Vegetation measurements and presence of a trapped animal were assumed to be independent from year to year because presence of small mammals depend heavily on annual growth of vegetation. For example, a single point in 1987 could have USE=1 and the same point in 1988 and/or 1989 have USE=0 for one species. The variable USE for each species was the response variable in the logistic regression models. The logit for the multiple logistic regression model is

$$g(x) = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \ldots + \beta_m x_m \qquad (9)$$

and the probability of use is

$$\pi(x) = \frac{e^{g(x)}}{1 + e^{g(x)}}. \qquad (10)$$

The predictor variables that were not found to be highly correlated in the multiple regression procedure were entered into the logistic regression routine in SPSS (ref) and the forward and backward selection routines were run on these parameters. The maximum iterations for maximum likelihood estimates were set at 20 and the significance level was 0.05. If a missing value was present in the data set the entire record associated with that

variable was thrown out. Therefore, each model that was selecte by the forward and backward selection process was run again in the logistic regression procedure of SPSS packages because more records were included in the parameter estimations. If the models selected by the forward and backward selection procedures were different and one was a reduced model of the second a log likelihood ratio test could be performed between the two. Wald's statistic, W_i, was used to test for the significance of each parameter included in the model where (Judge 1988)

$$W_i = \hat{\beta}_i^2/\hat{\sigma}^2 \quad . \qquad (11)$$

An example of model selection using Microtus longicaudus is included in appendix I.

RESULTS

Mammal Densities

There were 7,420 (21 species) small mammals captured over the three year trapping period (Table 1). A total of 2179 vegetation samples were measured over the study period. Means of the vegetation variables including the transformed variables are reported in tables 7-17.

Six species, Clethrionomys gapperi, Microtus longicaudus, Microtus montanus, Peromyscus maniculatis, Tamius minimus, and Zapus princeps, had a sufficient number of recaptures to compute the return rate (table 1) and probabilities of capture and recapture (table 2) in the Zippin model. The return rate for Clethrionomys gapperi, Peromyscus maniculatis, and Tamius minimus steadily increased over the trap nights, and the probabilities of

recapture were greater than the probabilities of first capture. The M_{bh} model in program CAPTURE was used to estimate abundances for these species and the Sorex species. Minimal behavior response was indicated with these measures for Microtus longicaudus, Microtus montanus, and Zapus princeps, therefore abundance estimates for these species were computed with the Lincoln-Peterson model. Means of the abundance estimates for these eight species are reported in tables 3 and 4. The width of the boundary strip (appendix E, table E.1) for each species in each habitat type was estimated and density estimates were calculated. Means of these estimates are reported in tables 5 and 6.

Repeated measures analysis

RMANOVA tables with p-values for the standard F-test, the H-F adjusted F-test, and the test for the H-F condition for Clethrionomys gapperi can be found in table 19. Following each ANOVA table are tables of the least square means including asterisks indicating the degree of statistical significance for the variables in that table. Figure one is plots of the least square means and associated p-values. Abundance estimators for Clethrionomys gapperi were not significantly different between the aspen, conifer or mixed plots ($p=0.11$). Clethrionomys gapperi abundances were significantly different in the north and south regions ($p<0.001$) and years ($p<.001$). However, there was a significant 2-way interaction between these two effects. The graph for this interaction term shows constant abundances in the

north region and a sharp decline in abundances in the south region over the three year period. These tables and figures for the remaining seven species are reported in appendix F.

Habitat selection functions

There were 22 variables (indicated by asterisks in tables 7-17) entered into the logistic regression forward and backward selection procedures. Highly correlated variables identified by the variance inflation factor and removed from the data set are listed in appendix E.

We attempted to build one habitat selection model for each habitat type in each region for each species, and was successful for Clethrionomys gapperi, Peromyscus maniculatis, Sorex cinereus, and Tamius minimus. However, most of the models for Microtus montanus, Microtus longicaudus, Zapus princeps, and Sorex monticolus did not converge or included only the intercept term indicating that none of the vegetation variables measured were significantly related to the probability of trapping an individual at that point. There were no significant differences in main effects for region or habitat in the repeated measures analysis for Microtus montanus, Microtus longicaudus, Zapus princeps. Therefore, a model for probability of use was built for each of these species from pooled data over habitat and region. Sorex monticolus had significant main effects and interactions for region and habitat in the repeated measures analysis, therefore no models were reported for this species.

Models built by the logistic regression forward and backward

selection procedures and associated log likelihoods for Clethrionomys gapperi are presented in tables 23-28. The steps in which the parameters were added or deleted in each model are reported in appendix H. These steps and models for the remaining seven species are reported in appendix G.

Variables measuring log features were most commonly selected in the habitat selection models. The varible MLDIST is a measure of the average distance to the closest log in each quarter of an eight meter radious circle, therefore this variable is presumed to be small if the logs are dense. This variable was selected in three habitat selection functions (north aspen, north mixed, and south aspen) and has a negative coefficient. Which means the probability of Clethrionomys gapperi selecting a point is higher when the logs are denser. In the north conifer and south mixed plots LOGAREA and LOGRAT were selected in the models. These variables represent the average number of logs in an eight meter radious circle, and the ratio between log diameter and distance to a log from the center point. Clethrionomys gapperi had positive selection for both of these parameters.

DISCUSSION

For most species capture and recapture data on each plot were inadequate for methods found in the literature on estimating abundance. Therefore, pooling data was required and a new technique developed using the Lincoln-Peterson estimate and the CAPTURE program. The procedure assumed that the data were pooled homogeneously. That is, the estimated probability of capturing

an animal at least once in the pooled data was the same for each plot pooled. The data were stratified by habitat and pooled over years, thus making this a reasonable assumption.

Determining the trapping tendencies in capture and recapture studies has always been a problem. To properly define an animal as trap happy or trap shy requires an estimated first capture probability and an estimated recapture probability. Small mammals that were captured in this study tend to be trap happy. Therefore, they were assumed to be trap happy unless otherwise indicated in the return rate estimates and Zippin model probabilities.

For most species there were variables with significant main effects in the repeated measures model. However, there were significant two-way or three-way interactions for these same variables in most cases. When this happens significance in the main effects may be misleading and interpretation should be made with caution.

The habitat selection functions presented in this paper have statistical significance and give some indication of the variables that are important. However, further investigation should be done such as interaction terms, variables known to be biologically important, weather data, etc. There has been no effort at this point to interpret the biological meaning of the parameters in each model. This is an important part of building these models and should be considered before significant relationships between the habitat variables and probability of

LITERATURE CITED

Clark, T. W., and Stromberg, M. R., 1987. Museum of Natural History, University of Kansas.

Cottam, G., J. T. Curtis, and B. W. Hale. 1953. Some sampling characteristics of a population of randomly dispersed individuals. Ecology 34, 741-757.

DeByle, N. V. 1985. Wildlife. Pages 135-152 in N. V. DeByle and R. Winokur (eds.), Aspen ecology and management in the United States. Rocky Mountain Forest and Range Experiment Station. USDA Forest Service General Technical Report RM-119.

Engeman, Richard M., D. E. Palmquist, and L. L. McDonald. 1985. The use of repeated measurement designs in field studies. Paper presented at the Symposium on statistical Analysis and Modeling of Grazing Systems, Orlando, FL.

Finch, D.M., R.T. Reynolds. 1988. Mammal community response to habitat variation and conifer succession in aspen forests. Study Plan RM-4201.1-1. Rocky Mountain Forest and Range Experiment Station, Fort Collins, CO.

Hosmer, D. W. Jr., and Lemeshow, S.. Applied Logistic Regression. John Wiley and Sons, Inc.. 1989.

Judge, G. G., Hill R. C., Griffiths, W. E., Lutkepohl, H., and Lee, T-C.. John Wiley and Sons, Inc.. 1988.

Lahey F77L version 4.10 Fortran 77 language system. 1990. Lahey Computer Systems Inc., Incline Village, NV.

Lotus 1-2-3. 1989. Lotus 1-2-3 reference. Lotus Development Corp. Cambridge, MA.

Lotus Freelance. 1988. Lotus freelance plus reference. Lotus Development corp. Cambridge, MA.

Manly, B.F.J., L.L. McDonald and L.L. Thomas. 1990. Resource selection functions. Preprint 591. Dept. of Statistics, University of Wyoming, Laramie.

Milliken G. A., Johnson D. E.. Analysis of messy data. Van Nostrand Reinhold. 1984.

McDonald, L.L., D.J. Reed, and W. Erickson. 1991. Analysis procedures for habitat and food selection studies. Pages 429-474 in C.E. Butler and S.P. Mahoney (eds.), Proceedings 4th North American caribou workshop. Newfoundland and Labrador Wildlife Division, St. John's, Newfoundland.

McDonald, L.L., B.F.J. Manly, and C.M. Raley. 1990. Analyzing foraging and habitat use through selection functions. In M.L. Morrison, C.J. Ralph, J. Verner and J.R. Jehl, Jr., (eds.), Mammal foraging: theory, methodology and applications. Studies in Mammal Biology No. 13, Cooper Ornithological Society, Suite 1400, 1100 Glendon Ave. Los Angeles.

Menkins, G. E., and S. H. Anderson 1988. Estimation of small Mammal population size. Ecology, 69, 1952-1959.

Mueller-Dombois, D., and Ellenberg, H.. 1974. Aims and methods

of vegetation ecology. John Wiley and Sons, Inc..

Otis, D. L., K. P. Burnham, G. C. White, and D. R. Anderson. 1978. Statistical inference from capture data on closed animal populations. Wildlife Monograph Number 62.

Pollard, J. H.. 1971. On distance estimators of density in randomly distributed forests. Biometrics 27, 991-1002.

Pollock, Kenneth H. 1991. Modeling capture, recapture, and removal statistics for estimation of demographic parameters for fish and wildlife populations: past, present and future. Journal of the American Statistical Association, 86, 225-238.

Pollock, K. H., and M. C. Otto 1983. Robust estimation of population size in closed animal populations from capture-recapture experiments. Biometrics, 39, 1035-1049.

RM/FORTRAN. 1987. RM/FORTRAN. Version 2.4. Ryan-McFarland Corporation. Torrance, CA.

Sarrazin J-P R, and Bider J. R.. Activity, a neglected parameter in population estimates-the development of a new technique. Journal of Mammalogy. vol. 54, 369-381.

SAS. 1989. SAS language and procedures. Version 6. SAS Institute. Cary, NC.

Seber, G. A. F. Estimation of Animal Abundance. Macmillan Publishing Company, Inc., New York, 1982.

Sheppe, W.,, The annual cycle of small mammal populations on a

Zambian floodplain. Journal of Mammalogy, vol 53, 445-460.

SPSS/PC. 1989. SPSS base manual. SPSS, Inc. Chicago, IL.

Summererlin, C. T., and Wolfe, J. L., Social influences on trap response of the cottonrat, Sigmodon hispidus. 1973. Ecology, vol.54, 1156-1159.

White, Gary C. 1991. User's manual for program capture. Department of Fishery and Wildlife Biology, Colorado State University, Fort Collins.

White, Gary C., David R. Anderson, Kenneth P. Burnham, David L. Otis. 1982. Capture-repcature and removal methods for sampling closed populations. Los Alamos National Laboratory Publication LA-8787-NERP.

Zippin, C., An Evaluation of the removal method of estimating animal populations. Biometrics 1956, vol. 12, 163-189.

Table 1. Return rates for six small mammal species captured in the central Rocky Mountains in 1987-1989. These numbers represent the ratio between the number of recaptures and the number of opportunities to be recaptured after a given night. The asterisk indicates those species not trap happy.

	TRAPPING NIGHT				
	1	2	3	4	5
Clethrionomys gapperi	0.350	0.451	0.573	0.705	0.875
Microtus longicaudus *	0.204	0.300	0.250	0.000	0.000
Microtus montanus *	0.121	0.278	0.571	0.500	0.000
Peromyscus maniculatis	0.481	0.581	0.641	0.745	0.807
Tamius minimus	0.297	0.457	0.641	0.631	0.733
Zapus princeps *	0.302	0.395	0.500	0.500	0.000

Table 2. Probabilities for first capture (p-hat) and recapture (c-hat) for six small mammal species captured in the central Rocky Mountains in 1987-1989. These probabilities were computed in the Zippin model in program CAPTURE (White et al. 1991). The asterisk indicates those species not trap happy.

	P-hat	C-hat	# captured
Clethrionomys gapperi			
ASPEN	0.034764	0.227590	1302
CONIFER	0.034756	0.257732	1277
MIXED	0.032024	0.257475	407
Microtus longicaudus*			
ASPEN	0.201520	0.125926	113
CONIFER	*	*	4
MIXED	0.272883	0.176471	29
Microtus montanus*			
ASPEN	*	*	133
CONIFER	0.333000	*	10
MIXED	0.185918	0.056338	32
Peromyscus maniculatis			
ASPEN	0.175036	0.421807	1130
CONIFER	0.029949	0.395349	56
MIXED	0.131171	0.522613	321
Tamius minimus			
ASPEN	0.179168	0.231099	709
CONIFER	0.288060	0.253731	44
MIXED	0.123495	0.289474	68
Zapus princeps*			
ASPEN	*	*	67
CONIFER	*	*	10
MIXED	0.263330	0.270270	12

Table 3. Mean abundance of small mammals for each habitat and year in the north region. The asterisk indicates those estimated with the Lincoln-Peterson estimator.

NORTH	1987 MEAN ABUNDANCE	1988 MEAN ABUNDANCE	1989 MEAN ABUNDANCE
Clethrionomys gapperi			
ASPEN	31.00	21.21	33.61
CONIFER	111.64	106.42	84.56
MIXED	13.71	8.07	28.23
Microtus longicaudus *			
ASPEN	0.00	0.28	4.42
CONIFER	0.00	0.43	0.00
MIXED	0.00	0.00	0.00
Microtus montanus *			
ASPEN	0.14	2.58	5.29
CONIFER	0.00	1.33	0.00
MIXED	0.44	0.00	2.66
Peromyscus maniculatis			
ASPEN	6.29	2.91	40.37
CONIFER	0.51	0.51	11.27
MIXED	14.38	5.33	55.42
Sorex cinereus			
ASPEN	17.50	9.48	19.69
CONIFER	76.98	20.87	65.23
MIXED	1.84	1.38	3.22
Sorex monticolus			
ASPEN	12.39	4.13	16.00
CONIFER	5.27	1.21	2.02
MIXED	1.05	0.00	2.63
Tamius minimus			
ASPEN	9.66	9.38	28.16
CONIFER	0.00	0.73	1.09
MIXED	0.59	0.59	8.87
Zapus princeps *			
ASPEN	0.00	0.32	1.29
CONIFER	0.67	0.00	0.00
MIXED	0.00	0.35	0.00

Table 4. Mean abundance estimates of small mammals for each habitat and year in the south region where the asterisk indicates those estimated with the Lincoln-Peterson estimator.

SOUTH		1987 MEAN ABUNDANCE	1988 MEAN ABUNDANCE	1989 MEAN ABUNDANCE
Clethrionomys gapperi				
	ASPEN	198.10	102.80	38.18
	CONIFER	171.03	98.34	34.68
	MIXED	147.64	104.88	25.81
Microtus longicaudus *				
	ASPEN	0.71	9.98	0.71
	CONIFER	0.00	1.28	0.00
	MIXED	0.37	8.97	1.49
Microtus montanus *				
	ASPEN	2.03	5.83	2.17
	CONIFER	0.67	0.67	0.67
	MIXED	2.66	7.55	0.89
Peromyscus maniculatis				
	ASPEN	45.59	48.04	30.24
	CONIFER	2.56	2.56	11.27
	MIXED	35.17	30.37	30.37
Sorex cinereus				
	ASPEN	172.86	45.22	132.75
	CONIFER	49.57	3.91	22.17
	MIXED	27.18	11.51	12.90
Sorex monticolus				
	ASPEN	27.62	11.10	40.01
	CONIFER	3.65	0.00	2.84
	MIXED	12.65	3.69	10.55
Tamius minimus				
TAMI	ASPEN	24.02	9.38	17.25
	CONIFER	4.01	4.01	6.56
	MIXED	8.28	13.01	8.87
Zapus princeps *				
ZAPR *	ASPEN	5.18	3.72	0.32
	CONIFER	2.67	0.00	0.00
	MIXED	0.35	3.52	0.00

Table 5. Mean density estimates of small mammals for each habitat and year in the north region. The asterisk indicates those estimated with the Lincoln-Peterson estimator.

NORTH	1987 MEAN DENSITY	1988 MEAN DENSITY	1989 MEAN DENSITY
Clethrionomys gapperi			
ASPEN	7.67	5.25	8.31
CONIFER	26.47	25.24	20.05
MIXED	3.46	2.04	7.13
Microtus longicaudus *			
ASPEN	0.00	0.08	1.25
CONIFER	0.00	0.16	0.00
MIXED	0.00	0.00	0.00
Microtus montanus *			
ASPEN	0.04	0.69	1.41
CONIFER	0.00	0.28	0.00
MIXED	0.14	0.00	0.86
Peromyscus maniculatis			
ASPEN	1.52	0.70	9.76
CONIFER	0.12	0.12	2.61
MIXED	3.26	1.21	12.54
Sorex cinereus			
ASPEN	2.98	1.61	3.35
CONIFER	17.35	4.70	14.70
MIXED	0.68	0.51	1.19
Sorex monticolus			
ASPEN	3.34	1.11	4.31
CONIFER	1.95	0.45	0.75
MIXED	0.33	0.00	0.82
Tamius minimus			
ASPEN	2.05	1.99	5.98
CONIFER	0.00	0.14	0.21
MIXED	0.12	0.12	1.82
Zapus princeps *			
ASPEN	0.00	0.06	0.26
CONIFER	0.13	0.00	0.00
MIXED	0.00	0.07	0.00

Table 6. Mean density estimates of small mammals for each habitat and year in the south region. The asterisk indicates those estimated with the Lincoln-Peterson etimator.

SOUTH	1987 MEAN DENSITY	1988 MEAN DENSITY	1989 MEAN DENSITY
Clethrionomys gapperi			
ASPEN	48.99	29.51	10.96
CONIFER	40.56	26.99	9.52
MIXED	37.29	30.80	7.58
Microtu longicaudus *			
ASPEN	0.20	3.31	0.24
CONIFER	0.00	0.57	0.00
MIXED	0.11	3.16	0.53
Microtus montanus *			
ASPEN	0.54	1.82	0.68
CONIFER	0.14	0.16	0.16
MIXED	0.86	2.91	0.34
Peromyscus maniculatis			
ASPEN	11.02	13.46	8.47
CONIFER	0.59	0.68	3.01
MIXED	7.96	7.93	7.93
Sorex cinereus			
ASPEN	29.42	8.71	25.57
CONIFER	11.17	1.02	5.76
MIXED	10.07	5.12	5.73
Sorex monticolus			
ASPEN	7.45	3.50	12.60
CONIFER	1.35	0.00	1.26
MIXED	3.94	1.36	3.88
Tamius minimus			
ASPEN	5.10	2.29	4.21
CONIFER	0.78	0.89	1.46
MIXED	1.70	3.06	2.09
Zapus princeps *			
ASPEN	1.02	0.84	0.07
CONIFER	0.53	0.00	0.00
MIXED	0.07	0.84	0.00

Table 7. Average percent shrub cover and average percent frequency of shrubs on line intercept. Average percent canopy cover, and average grass and forb percent cover for each habitat, year and region. Computations and pooling are outlined in Appendix B. The asterisks indicate which variabes were included in the logistic regression selection procedure.

			NORTH			SOUTH		
			ASPEN	CONIFER	MIXED	ASPEN	CONIFER	MIXED
PCOVER	87		6.1	8.8	1.5	.	.	.
	88		7.8	15.7	1.4	7.2	7.0	4.4
	89		9.3	18.1	2.2	8.3	8.0	8.0
PCONCOV	87	*	7.9	5.6	5.5	.	.	.
	88		4.5	5.2	1.9	2.3	5.6	5.1
	89		6.5	5.3	4.0	0.4	6.6	13.5
PDECCOV	87	*	7.8	9.1	3.2	.	.	.
	88		9.8	22.4	2.9	9.8	7.9	7.8
	89		10.7	20.8	2.8	11.9	9.9	8.0
POTHCOV	87	*	4.9	1.4	1.2	.	.	.
	88		.	.	7.5	.	.	.
	89		1.3	3.2	1.8	1.8	1.4	2.6
PPOTRCV	87	*	1.2	.	2.7	.	.	.
	88		1.7	.	2.6	1.0	2.7	1.3
	89		2.5	.	2.1	1.6	0.6	1.8
PFQCON	87		.	.	.	.	.	.
	88		39.3	16.0	30.4	14.3	27.0	18.8
	89		23.1	31.1	23.9	23.7	21.2	30.4
PFQDEC	87		.	.	.	.	.	.
	88		24.7	36.3	23.6	11.6	33.5	16.4
	89		24.2	31.5	26.6	19.9	43.6	29.2
PFQOTH	87		.	.	.	.	.	.
	88		.	.	10.0	.	.	.
	89		10.0	80.0	66.7	25.5	35.3	38.7
PFQPOTR	87		.	.	.	.	.	.
	88		21.6	.	20.0	20.5	20.0	26.3
	89		24.3	.	22.4	26.1	29.2	23.3
CCAVE	87	*	61.1	61.8	57.2	.	.	.
	88		43.7	47.8	51.3	83.9	80.5	77.1
	89		72.2	66.5	73.8	84.9	81.4	81.5
GRFBS	87	*	28.4	24.0	22.4	.	.	.
	88		47.6	23.1	36.4	29.5	22.4	24.3
	89		46.6	32.2	30.1	26.4	21.4	24.8

PCOVER - percent shrub cover
PCONCOV - percent conifer shrub cover
PDECCOV - percent mast and fruit producing deciduous shrub cover
PPOTRCV - percent aspen shrub cover
POTHCOV - percent other deciduous shrub cover
PFQCON - percent frequency of conifer shrubs
PFQDEC - percent frequency of mast and fruit producing deciduous shrubs
PFQOTH - percent frequency of other deciduous shrubs
PFQPOTR - percent frequency of quaken aspen shrubs
CCAVE - average canopy closure
GRFBS - percent grass and forb cover

Table 8. Mean diameter (cm) for trees and logs, and mean distances (cm) from center of sample point to trees and logs for each habitat, year in the north region. Computations are outlined in Appendix B. The asterisks indicate which variables were included in the logistic regression selection procedure.

			NORTH					
			ASPEN		CONIFER		MIXED	
			MEAN	STD	MEAN	STD	MEAN	STD
MTDIAM	87	*	24.8	5.6	32.4	8.4	26.3	6.4
	88		24.9	5.4	33.2	5.8	25.5	6.0
	89		24.3	4.8	34.1	6.3	25.1	5.3
MLDIAM	87	*	15.0	3.7	19.2	6.7	13.7	2.2
	88		19.0	4.9	28.8	10.7	15.5	3.9
	89		14.6	3.7	20.3	10.6	14.4	4.5
MABLADM	87		.	.	28.1	8.0	19.9	4.7
	88		39.4	.	28.4	6.7	17.8	2.0
	89		19.2	3.8	29.2	7.6	17.7	2.2
MPOTRDM	87		24.8	5.6	.	.	23.7	5.3
	88		24.8	5.4	.	.	22.0	4.2
	89		24.4	4.9	.	.	23.1	5.5
MPICODM	87		.	.	27.7	7.1	31.0	11.6
	88		.	.	.	.	32.9	12.8
	89		.	.	27.9	6.5	31.3	13.1
MPIENDM	87		.	.	37.8	13.8	.	.
	88		.	.	37.0	9.1	.	.
	89		20.0	.	40.2	11.7	.	.
MTDIST	87	*	501.8	209.9	437.3	161.3	480.9	344.2
	88		544.5	206.8	472.7	148.8	630.3	762.6
	89		467.4	210.0	492.3	287.7	482.8	288.4
MLDIST	87	*	469.9	334.2	335.0	166.4	910.5	791.0
	88		681.7	436.9	509.7	318.7	870.1	692.9
	89		253.2	166.6	209.6	178.2	330.4	181.3
MABLADST	87		.	.	479.3	207.6	394.8	203.6
	88		754.5	.	501.4	172.6	631.3	1134.8
	89		514.0	458.2	485.6	293.0	433.0	290.4
MPOTRDST	87		501.8	209.9	.	.	496.2	500.5
	88		542.6	208.4	.	.	605.5	746.2
	89		467.2	209.0	.	.	486.3	377.0
MPICODST	87		.	.	393.3	233.9	545.2	388.2
	88		.	.	.	.	794.9	1184.9
	89		.	.	525.2	177.8	503.3	351.1
MPIENDST	87		.	.	395.8	203.0	.	.
	88		.	.	471.5	235.9	.	.
	89		1599.0	.	507.4	424.2	.	.

MTDIAM - mean tree diameter
MLDIAM - mean log diameter
MABLADM - mean diameter for subalpine fir
MPOTRDM - mean diameter for quaken aspen
MPICODM - mean diameter for lodgepole pine
MPIENDM - mean diameter for engelman spruce
MTDIST - mean tree distance
MLDIST - mean log distance
MABLADST - mean distance for subalpine fir
MPOTRDST - mean distance for quaken aspen
MPICODST - mean distance for lodgepole pine
MPIENDST - mean distance for engelman spruce

Table 9. Mean diameter (cm) for trees and logs, and mean distances (cm) from center of sample point to trees and logs for each habitat, year in the south region. Computations are outlined in Appendix B. The asterisks indicate which variables were included in the logistic regression selection procedures.

			SOUTH					
			ASPEN		CONIFER		MIXED	
			MEAN	STD	MEAN	STD	MEAN	STD
MTDIAM	87	*	.	.	.	.	.	.
	88		23.2	4.3	32.0	7.2	30.5	9.2
	89		24.1	4.6	30.6	6.9	29.6	7.4
MLDIAM	87	*	.	.	.	.	.	.
	88		10.2	5.3	19.7	8.8	15.6	9.2
	89		12.6	5.4	18.7	9.2	11.9	5.7
MABLADM	87		.	.	.	.	.	.
	88		.	.	27.7	7.5	31.7	12.6
	89		.	.	26.7	7.4	30.0	12.7
MPOTRDM	87		.	.	.	.	.	.
	88		23.2	4.3	37.0	10.2	28.1	8.1
	89		24.1	4.6	35.6	12.4	27.3	8.0
MPICODM	87		.	.	.	.	.	.
	88		.	.	.	.	.	.
	89		.	.	.	.	.	.
MPIENDM	87		.	.	.	.	.	.
	88		.	.	36.7	12.0	44.3	21.4
	89		.	.	32.6	11.3	48.9	17.9
MTDIST	87	*	.	.	.	.	.	.
	88		385.6	179.0	385.1	129.7	502.7	263.9
	89		441.8	250.2	381.6	137.6	502.6	248.7
MLDIST	87	*	.	.	.	.	.	.
	88		242.4	174.2	192.1	126.6	288.7	206.3
	89		248.1	188.3	256.3	146.4	343.4	189.3
MABLADST	87		.	.	.	.	.	.
	88		.	.	376.9	156.9	516.6	316.9
	89		.	.	385.1	177.8	533.6	321.0
MPOTRDST	87		.	.	.	.	.	.
	88		385.6	179.0	408.6	225.7	504.1	302.3
	89		441.3	250.5	420.3	207.0	536.8	281.9
MPICODST	87		.	.	.	.	.	.
	88		.	.	.	.	.	.
	89		.	.	.	.	.	.
MPIENDST	87		.	.	.	.	.	.
	88		.	.	387.3	171.6	595.1	448.1
	89		.	.	390.8	169.9	510.6	388.4

MTDIAM - mean tree diameter
MLDIAM - mean log diameter
MABLADM - mean diameter for subalpine fir
MPOTRDM - mean diameter for quaken aspen
MPICODM - mean diameter for lodgepole pine
MPIENDM - mean diameter for engelman spruce
MTDIST - mean tree distance
MLDIST - mean log distance
MABLADST - mean distance for subalpine fir
MPOTRDST - mean distance for quaken aspen
MPICODST - mean distance for lodgepole pine
MPIENDST - mean distance for engelman spruce

LIBRARY COPY
ROCKY MTN. FOREST & RANGE
EXPERIMENT STATION

Table 10. Average ration between mean diameter and mean distance for trees and logs, and average herb and shrub frequency from the horizontal profile at .5 meters and 1.5 meters height for each habitat and year in the north region. Computations are outlined in Appendix B. The asterisks indicate which variables were included in the logistic regression selection procedures.

			NORTH					
			ASNEN		CONIFER		MIXED	
			MEAN	STD	MEAN	STD	MEAN	STD
TREERAT	87	*	0.057	0.026	0.083	0.037	0.068	0.027
	88		0.052	0.022	0.080	0.037	0.066	0.030
	89		0.061	0.024	0.084	0.036	0.067	0.039
LOGRAT	87	*	0.058	0.061	0.079	0.088	0.039	0.064
	88		0.041	0.035	0.071	0.043	0.035	0.044
	89		0.108	0.118	0.156	0.190	0.076	0.100
ABLARAT	87		.	.	0.069	0.033	0.063	0.034
	88		0.052	.	0.064	0.029	0.117	0.178
	89		0.057	0.043	0.083	0.056	0.058	0.034
POTRRAT	87		0.057	0.026	.	.	0.071	0.042
	88		0.052	0.022	.	.	0.066	0.042
	89		0.061	0.024	.	.	0.069	0.049
PICORAT	87		.	.	0.098	0.076	0.082	0.082
	88		.	.	.	.	0.082	0.056
	89		.	.	0.056	0.016	0.108	0.141
PIENRAT	87		.	.	0.145	0.148	.	.
	88		.	.	0.105	0.066	.	.
	89		0.013	.	0.120	0.090	.	.
MHFQ2	87	*	2.287	2.142	2.500	3.335	1.301	1.362
	88		4.942	9.509	3.778	5.815	2.569	4.066
	89		2.494	3.489	0.496	1.319	0.466	0.931
MSFQ2	87	*	0.873	1.489	0.083	0.146	0.317	0.903
	88		2.186	3.272	0.270	0.456	1.114	2.213
	89		0.789	1.286	0.044	0.207	0.232	0.463
MHFQ3	87	*	0.010	0.056	0.000	0.000	0.000	0.000
	88		0.075	0.621	0.032	0.146	0.008	0.052
	89		0.003	0.031	0.000	0.000	0.003	0.031
MSFQ3	87	*	0.082	0.261	0.014	0.067	0.000	0.000
	88		0.272	1.029	0.175	0.801	0.203	0.996
	89		0.130	0.381	0.006	0.045	0.084	0.602

TREERAT - mean tree diameter divided by mean tree distance
LOGRAT - mean log diameter divided by mean log distance
ABLARAT - mean subalpine fir diameter divided by mean subalpine fir distance
POTRRAT - mean quaken aspen diameter divided by mean quaken aspen distance
PICORAT - mean lodgepole pine diameter divided by mean lodgepole pine distance
PIENRAT - mean engelman spruce diameter divided by mean engelman spruce distance
MHFR2 - average herb frequency at 0.5 meters
MHFR3 - average herb frequency at 1.5 meters
MSFR2 - average shrub frequency at 0.5 meters
MSFR3 - average shrub frequency at 1.5 meters

Table 11. Average ration between mean diameter and mean distance for trees and logs, and average herb and shrub frequency from the horizontal profile at .5 meters and 1.5 meters height for each habitat and year in the south region. Computations are outlined in Appendix B. The asterisks indicate which variables were included in the logistic regression selection procedures.

			SOUTH					
			ASPEN		CONIFER		MIXED	
			MEAN	STD	MEAN	STD	MEAN	STD
TREERAT	87	*	.	.	.	.	.	.
	88		0.072	0.035	0.091	0.031	0.075	0.039
	89		0.068	0.036	0.088	0.030	0.076	0.051
LOGRAT	87	*	.	.	.	.	.	.
	88		0.057	0.052	0.185	0.253	0.082	0.094
	89		0.091	0.112	0.117	0.137	0.043	0.041
ABLARAT	87		.	.	.	.	.	.
	88		.	.	0.086	0.043	0.090	0.082
	89		.	.	0.083	0.046	0.079	0.052
POTRRAT	87		.	.	.	.	.	.
	88		0.072	0.035	0.139	0.141	0.089	0.166
	89		0.068	0.036	0.098	0.048	0.069	0.043
PICORAT	87		.	.	.	.	.	.
	88		.	.	.	.	.	.
	89		.	.	.	.	.	.
PIENRAT	87		.	.	.	.	.	.
	88		.	.	0.115	0.079	0.125	0.114
	89		.	.	0.101	0.061	0.148	0.114
MHFQ2	87	*	.	.	.	.	.	.
	88		1.303	1.462	0.347	0.763	1.030	1.110
	89		3.143	2.606	0.772	2.101	1.538	1.416
MSFQ2	87	*	.	.	.	.	.	.
	88		0.752	1.493	0.448	0.609	0.574	1.093
	89		0.327	0.717	0.032	0.163	0.273	0.592
MHFQ3	87	*	.	.	.	.	.	.
	88		0.022	0.101	0.000	0.000	0.031	0.165
	89		0.003	0.032	0.000	0.000	0.000	0.000
MSFQ3	87	*	.	.	.	.	.	.
	88		0.068	0.296	0.087	0.417	0.026	0.142
	89		0.020	0.134	0.000	0.000	0.000	0.000

TREERAT - mean tree diameter divided by mean tree distance
LOGRAT - mean log diameter divided by mean log distance
ABLARAT - mean subalpine fir diameter divided by mean subalpine fir distance
POTRRAT - mean quaken aspen diameter divided by mean quaken aspen distance
PICORAT - mean lodgepole pine diameter divided by mean lodgepole pine distance
PIENRAT - mean engelman spruce diameter divided by mean engelman spruce distance
MHFR2 - average herb stem frequency at 0.5 meters
MHFR3 - average herb stem frequency at 1.5 meters
MSFR2 - average shrub stem frequency at 0.5 meters
MSFR3 - average shrub stem frequency at 1.5 meters

Table 12. Mean number of live and dead trees relative to area searched (8 meter radious circle) and average litter depth for each habitat and year in the north region. Computations are outlined in Appendix B. The asterisks indicate which variables wre included in the logistic regression selection procedure.

			NORTH					
			ASPEN		CONIFER		MIXED	
			MEAN	STD	MEAN	STD	MEAN	STD
LIVEAREA	87	*	0.095	0.053	0.070	0.033	0.211	0.106
	88		0.090	0.046	0.065	0.031	0.202	0.108
	89		0.121	0.061	0.066	0.031	0.162	0.062
DEADAREA	87	*	0.023	0.023	0.019	0.023	0.046	0.042
	88		0.020	0.021	0.017	0.015	0.047	0.046
	89		0.028	0.025	0.019	0.018	0.044	0.036
LABLA	87	*	0.001	0.006	0.036	0.025	0.043	0.089
	88		0.001	0.007	0.032	0.026	0.048	0.080
	89		0.001	0.004	0.032	0.021	0.029	0.044
DABLA	87	*	0.000	0.000	0.015	0.022	0.001	0.009
	88		0.000	0.000	0.011	0.011	0.003	0.012
	89		0.000	0.000	0.013	0.016	0.001	0.003
LPOTR	87	*	0.084	0.045	0.000	0.000	0.062	0.033
	88		0.088	0.045	0.000	0.000	0.068	0.048
	89		0.096	0.038	0.000	0.000	0.058	0.038
DPOTR	87	*	0.022	0.022	0.000	0.000	0.028	0.025
	88		0.020	0.021	0.000	0.000	0.031	0.037
	89		0.025	0.023	0.000	0.000	0.037	0.033
LPIEN	87	*	0.000	0.000	0.033	0.023	0.000	0.000
	88		0.000	0.000	0.033	0.026	0.000	0.000
	89		0.000	0.000	0.034	0.026	0.000	0.000
DPIEN	87	*	0.000	0.000	0.003	0.005	0.000	0.000
	88		0.000	0.000	0.006	0.009	0.000	0.000
	89		0.000	0.000	0.006	0.011	0.000	0.000
LPICO	87	*	0.000	0.000	0.002	0.004	0.107	0.068
	88		0.000	0.000	0.001	0.003	0.085	0.056
	89		0.000	0.000	0.000	0.002	0.075	0.050
DPICO	87	*	0.000	0.000	0.001	0.002	0.016	0.021
	88		0.000	0.000	0.000	0.000	0.013	0.016
	89		0.000	0.000	0.000	0.001	0.006	0.008
AVLITTER	87	*	1.639	1.020	2.907	4.739	4.242	2.807
	88		2.675	2.186	2.323	1.929	3.257	2.062
	89		2.000	1.658	2.692	3.270	2.065	1.417

LIVEAREA - live stems / area searched
DEADAREA - dead stems /area searched
LOGAREA - log frequency / area searched
LABLA - live subalpine fir / area searched
DABLA - dead subalpine fir / area searched
LPOTR - live aspen / area searched
DPOTR - dead aspen / area searched
LPICO - live lodgepole pine / area searched
DPICO - dead lodgepole pine / area searched
LPIEN - live engelman spruce / area searched
DPIEN - dead engelman spruce / area searched
AVLITTER - average litter depth

Table 13. Mean number of live and dead trees relative to area searched (8 meter radious circle), and average litter depth for each habitat and year in the south region. Computations are outlined in Appendix B. The asterisks indicate which variables were included in the logistic regression selection prodedure.

			SOUTH					
			ASPEN		CONIFER		MIXED	
			MEAN	STD	MEAN	STD	MEAN	STD
LIVEAREA	87	*	.	.	.	.	.	.
	88		0.154	0.084	0.108	0.047	0.100	0.054
	89		0.141	0.083	0.116	0.070	0.113	0.067
DEADAREA	87	*	.	.	.	.	.	.
	88		0.046	0.044	0.024	0.025	0.022	0.022
	89		0.038	0.032	0.039	0.040	0.022	0.024
LABLA	87	*	.	.	.	.	.	.
	88		0.000	0.001	0.071	0.048	0.036	0.029
	89		0.000	0.001	0.064	0.061	0.050	0.049
DABLA	87	*	.	.	.	.	.	.
	88		0.000	0.000	0.020	0.026	0.008	0.015
	89		0.000	0.000	0.026	0.036	0.008	0.012
LPOTR	87	*	.	.	.	.	.	.
	88		0.141	0.079	0.009	0.012	0.056	0.050
	89		0.137	0.082	0.009	0.011	0.052	0.034
DPOTR	87	*	.	.	.	.	.	.
	88		0.045	0.044	0.002	0.004	0.014	0.018
	89		0.038	0.032	0.003	0.005	0.013	0.015
LPIEN	87	*	.	.	.	.	.	.
	88		0.000	0.001	0.029	0.022	0.007	0.012
	89		0.000	0.000	0.044	0.032	0.009	0.015
DPIEN	87	*	.	.	.	.	.	.
	88		0.000	0.000	0.002	0.004	0.000	0.001
	89		0.000	0.000	0.011	0.015	0.001	0.004
LPICO	87	*	.	.	.	.	.	.
	88		0.000	0.000	0.000	0.000	0.000	0.000
	89		0.000	0.000	0.000	0.000	0.000	0.000
DPICO	87	*	.	.	.	.	.	.
	88		0.000	0.000	0.000	0.000	0.000	0.000
	89		0.000	0.000	0.000	0.000	0.000	0.000
AVLITTER	87	*	.	.	.	.	.	.
	88		2.438	1.505	2.405	3.503	2.278	2.364
	89		1.884	1.276	2.009	1.786	1.735	1.546

LIVEAREA - live stems / area searched
DEADAREA - dead stems /area searched
LOGAREA - log frequency / area searched
LABLA - live subalpine fir / area searched
DABLA - dead subalpine fir / area searched
LPOTR - live aspen / area searched
DPOTR - dead aspen / area searched
LPICO - live lodgepole pine / area searched
DPICO - dead lodgepole pine / area searched
LPIEN - live engelman spruce / area searched
DPIEN - dead engelman spruce / area searched
AVLITTER - average litter depth

Table 14. Frequency table for the categorical variable, STEMTYPE, indicating the type of trees present at each point in each habitat, region and year.

STEM TYPE		ASPEN			CONIFER			MIXED		
		87	88	89	87	88	89	87	88	89
NORTH	ASPEN	110	118	126	.	.	.	2	2	.
	CONIFER	.	.	.	36	31	52	.	1	.
	OTHER DECID	.	.	.	.	.	.	.	.	.
	MIXED	35	12	104	.	.	.	56	55	115
	NO STEMS	.	1	1	.	.	1	.	.	.
SOUTH	ASPEN	.	103	182	.	.	.	.	5	.
	CONIFER	.	.	.	.	50	33	.	5	.
	OTHER DECID	.	.	.	.	.	.	.	1	.
	MIXED	.	56	35	.	50	45	.	106	46
	NO STEMS	.	.	1	.	.	.	.	.	.

STEMTYPE 0=no stems present
1=all apsen
2=all conifer
3=all other deciduous
4=mixed

Table 15. Frequency table for the categorical variable, LIVEDEAD, indicating whether all trees present at a sample point are alive, dead, or both for each habitat, year, and region.

LIVE/DEAD STEMS		ASPEN			CONIFER			MIXED		
		87	88	89	87	88	89	87	88	89
NORTH	LIVE	.	.	159	.	.	20	.	.	78
	DEAD	.	.	1	.	.	.	.	.	.
	LV & DD	.	.	71	.	.	33	.	.	37
	NO STEMS	145	131	.	36	31	.	58	58	.
SOUTH	LIVE	.	140	174	.	45	30	.	73	35
	DEAD	.	.	.	.	.	.	.	.	.
	LV & DD	.	17	44	.	51	47	.	38	10
	NO STEMS	.	2	.	.	4	1	.	6	1

LIVEDEAD 1=all stems measured are live
2=all stems measured are dead
3=measured live and dead stems
4=variable not recorded

TABLE 18. Estimated density of trees on each plot in each forest type, region, and year using the point-quarter-circle-sampling-method (Pollard 1971).

		NORTH		
		ASPEN	CONIFER	MIXED
TDEN	87	0.37	0.54	0.47
	88	0.37	0.46	0.15
	89	0.42	0.48	0.41
POTRDEN	87	0.37	0.00	0.26
	88	0.37	0.00	0.08
	89	0.42	0.00	0.24
ABLADEN	87	0.00	0.24	0.04
	88	0.00	0.18	0.01
	89	0.00	0.24	0.02
PICODEN	87	0.00	0.04	0.17
	88	0.00	0.02	0.06
	89	0.00	0.05	0.14
PIENDEN	87	0.00	0.26	0.00
	88	0.00	0.25	0.00
	89	0.00	0.19	0.00

		SOUTH		
		ASPEN	CONIFER	MIXED
TDEN	87	.	.	.
	88	0.54	0.61	0.29
	89	0.49	0.61	0.34
POTRDEN	87	.	.	.
	88	0.54	0.05	0.18
	89	0.49	0.05	0.19
ABLADEN	87	.	.	.
	88	0.00	0.33	0.09
	89	0.00	0.32	0.10
PICODEN	87	.	.	.
	88	0.00	0.00	0.00
	89	0.00	0.00	0.00
PIENDEN	87	.	.	.
	88	0.00	0.22	0.03
	89	0.00	0.24	0.04

1. TDEN - stem density pooled over all trees
2. ABLADEN - stem density for subalpine fir
3. POTRDEN - stem density for quaken aspen
4. PICODEN - stem density for lodgepole pine
5. PIENDEN - stem density for engelman spruce

Table 16. Frequency count for the categorical variable, DOCO, indicating the dominance and codominance of grass and sedge for each habitat, year and region.

GRASS OR SEDGE		ASPEN			CONIFER			MIXED		
		87	88	89	87	88	89	87	88	89
NORTH	GR/GR	110	50	182	25	24	49	19	12	45
	GR/SE	14	30	19	6	3	.	10	1	17
	SE/SE	.	.	.	.	.	.	1	.	.
	SE/GR	21	51	30	5	4	4	28	45	53
SOUTH	GR/GR	.	66	94	.	42	30	.	88	32
	GR/SE	.	37	56	.	3	5	.	10	3
	SE/SE	.	.	.	.	.	.	.	.	.
	SE/GR	.	56	68	.	55	43	.	19	11

DOCO - 1=grass dominant, grass co-dominant
2=grass dominant, sedge co-dominant
3=sedge dominant, sedge co-dominant
4=sedge dominant, grass co-dominant

Table 17. Frequency count for the categorcial variable, SOILTYPE, indicating the main type of soil present at each point for each habitat, year and region.

SOIL TYPE		ASPEN			CONIFER			MIXED		
		87	88	89	87	88	89	87	88	89
NORTH	ROCK	.	.	.	1	.	1	.	.	.
	GRAVEL	.	.	.	.	.	.	.	.	1
	SAND	53	.	.	.	.	.	51	.	.
	CLAY	92	.	24	35	.	1	7	.	.
	LOAM	.	131	207	.	31	51	.	58	114
SOUTH	ROCK	.	.	.	.	.	.	.	.	.
	GRAVEL	.	.	1	.	.	.	.	.	.
	SAND	.	.	.	.	.	3	.	.	.
	CLAY	.	.	.	.	1	.	.	.	2
	LOAM	.	159	217	.	99	75	.	117	44

SOILTYPE - 1=rock
2=gravel
3=sand
4=clay
5=loam

Table 19. Repeated measures analysis of variance table for Clethrionomys gapperi abundances in aspen, conifer and mixed tree types in two regions for the years 1987-1989.

SOURCE	DF	TYPE III SS	MS	F	Pr > F	HF Adj Pr > F
REG	1	49992.43	49992.43	11.73	0.00	
HAB	2	20458.70	10229.35	2.40	0.11	
REG*HAB	2	24360.67	12180.33	2.86	0.08	
ERROR(PLOT)	24	102328.90	4263.70			
YEAR	2	59023.91	29511.95	11.99		0.00
YEAR*REG	2	53630.66	26815.33	10.90		0.00
YEAR*HAB	4	2765.71	691.43	0.28		0.88
YEAR*REG*HAB	4	2871.85	717.96	0.29		0.88
ERROR(YEAR)	48	118116.40	2460.76			

Huynh-Feldt Epsilon = 0.9666

DF - degrees of freedom

TYPE III SS - Type III sum of squares

MS - mean square

F- F-value for standard F-test

Pr>F - p-value for standard F-test

HF adj Pr>F - p-value for Huynh-Feltd adjusted F-test

Huynh-Feldt epsilon- A test for compound symmetry. If this value is less than one an adjustment in the degrees of freedom for the F-test is made.

Table 20. Least square means for Clethrionomys gapperi

	1987	1988	1989
NORTH ASPEN	31.00	21.21	33.62
NORTH CONIFER	111.65	106.42	84.57
NORTH MIXED	13.72	8.07	28.24
SOUTH ASPEN	198.10	102.80	38.18
SOUTH CONIFER	171.04	98.35	34.68
SOUTH MIXED	147.65	104.89	25.82

	1987	1988	1989
ASPEN	114.55	62.01	35.90
CONIFER	141.35	102.39	59.63
MIXED	80.68	56.48	27.03

***	1987	1988	1989
NORTH	52.12	45.24	48.81
SOUTH	172.26	102.01	32.90

***	1987	1988	1989
MARGINAL MEAN	112.19	73.62	40.85

	ASPEN	CONIFER	MIXED
NORTH	28.61	100.88	16.67
SOUTH	113.03	101.36	92.78

	ASPEN	CONIFER	MIXED
MARGINAL MEAN	70.82	101.12	54.73

***	NORTH	SOUTH
MARGINAL MEAN	48.72	102.39

GRAND MEAN	75.56

* significant at .05 level
*** significant at .001 level

Figure 1. Graphs of least square means for Tamius minimus abundances.

YEAR*REGION*HABITAT
(P=0.88 for 3-way interaction)

YEAR*HABITAT
(P=0.88 for 2-way interaction)

YEAR*REGION
(p<0.001 for 2-way interaction)

YEAR
(p<0.001 for main effects)

Figure 1 cont'd. Graphs of least square means for Tamias minimus abundances.

REGION*HABITAT
(P=0.08 for 2-way interaction)

HABITAT
(P=0.11 for main effects)

REGION
(p<0.001 for main effects)

Table 23. Estimated Habitat Selection Function models for Clethrionomys gapperi in the Aspen habitat of the north region built with Logistic regression forward and backward selection routines in SPSS packages.

* Forward selection -2 Log Likelihood 626.281

Variable	B	S.E.	Wald	Sig
AVLITTER	.1944	.0564	11.8916	.0006
MLDIST	-.0015	.0004	13.1536	.0003
MLDIAM	.0548	.0222	6.1197	.0134
Constant	-2.3334	.3911	35.5948	.0000

Backward selection -2 Log Likelihood 621.045

Variable	B	S.E.	Wald	Sig
AVLITTER	.1867	.0562	11.0227	.0009
MLDIAM	.0630	.0226	7.7598	.0053
MLDIST	-.0013	.0004	10.5329	.0012
STEM3	.4869	.2124	5.2569	.0219
STEM4	-1.0532	13.5140	.0061	.9379
Constant	-2.6971	.4281	39.6940	.0000

Log likelihood ratio test: 626.281 - 621.045 = 5.236
d.f.: 4
p-value: 0.2523
model: forward selection

Table 24. Estimated Habitat Selection Function models for Clethrionomys gapperi in the Conifer habitat of the north region built with Logistic regression forward and backward selection routines in SPSS packages.

* Forward selection -2 Log Likelihood 258.210

Variable	B	S.E.	Wald	Sig
LOGAREA	17.6289	5.2510	11.2712	.0008
PDECCOV	.0281	.0110	6.5865	.0103
Constant	-.4256	.3866	1.2123	.2709

Backward selection -2 Log Likelihood 244.880

Variable	B	S.E.	Wald	Sig
CCAVE	-.0371	.0112	10.9651	.0009
GG	-.8282	.5222	2.5148	.1128
LOGAREA	13.8482	5.1219	7.3102	.0069
MTDIST	-.0031	.0011	7.5580	.0060
LOGRAT	3.7845	1.9844	3.6370	.0565
Constant	4.2301	1.1575	13.3560	.0003

able 25. Estimated Habitat Selection Function models for Clethrionomys gapperi in the Mixed habitat of the north region built with Logistic regression forward and backward selection routines in SPSS packages.

Forward selection -2 Log Likelihood 200.026

Variable	B	S.E.	Wald	Sig
TREERAT	12.1274	5.0046	5.8721	.0154
Constant	-2.5651	.4145	38.2922	.0000

Backward selection -2 Log Likelihood 190.091

Variable	B	S.E.	Wald	Sig
MLDIST	-.0012	.0006	4.4938	.0340
TREERAT	8.8041	5.0864	2.9960	.0835
Constant	-1.6708	.5109	10.6972	.0011

Log likelihood ratio test: 200.026 - 190.091 = 9.935
d.f.: 1
p-value: 0.0016
model: backward selection

Table 26. Estimated Habitat Selection Function models for Clethrionomys gapperi in the Aspen habitat of the south region built with Logistic regression forward and backward selection routines in SPSS packages.

Forward selection -2 Log Likelihood 531.619

Variable	B	S.E.	Wald	Sig
STEM2	-4.4822	15.4189	.0845	.7713
STEM3	.7602	.2155	12.4469	.0004
STEM4	-4.4961	22.2402	.0409	.8398
MHFQ2	-.2097	.0581	13.0075	.0003
MSFQ2	3.9837	1.6229	6.0256	.0141
Constant	-.9339	.1795	27.0828	.0000

Backward selection -2 Log Likelihood 509.690

Variable	B	S.E.	Wald	Sig
GRFBS	.0092	.0051	3.3002	.0693
MHFQ2	-.2229	.0604	13.6204	.0002
MSFQ2	4.1281	1.6487	6.2691	.0123
MLDIAM	.0388	.0219	3.1343	.0767
MLDIST	-.0015	.0007	4.7816	.0288
STEM2	-4.8690	15.3585	.1005	.7512
STEM3	.8067	.2371	11.5747	.0007
STEM4	-4.2635	22.2421	.0367	.8480
Constant	-1.2745	.3502	13.2427	.0003

Log likelihood ratio test: 531.619 - 190.091 = 21.926
d.f.: 3
p-value: 0.0001
model: backward selection

Table 27. Estimated Habitat Selection Function models for Clethrionomys gapperi in the Conifer habitat of the south region built with Logistic regression forward and backward selection routines in SPSS packages.

Forward selection -2 Log Likelihood 128.109

Variable	B	S.E.	Wald	Sig
STEM1	1.2133	.4445	7.4510	.0063
MHFQ3	1.3826	.5906	5.4798	.0192
Constant	-1.4754	.3860	14.6095	.0001

Backward selection -2 Log Likelihood 126.150

Variable	B	S.E.	Wald	Sig
STEM1	1.2194	.4502	7.3377	.0068
MHFQ3	1.6727	.6611	6.4020	.0114
PCONCOV	-.0571	.0417	1.8740	.1710
Constant	-1.3484	.4001	11.3572	.0008

Log likelihood ratio test: 128.109 - 126.151 = 1.959
d.f.: 1
p-value: 0.1616
model: forward selection

Table 28. Estimated Habitat Selection Function models for Clethrionomys gapperi in the Mixed habitat of the south region built with Logistic regression forward and backward selection routines in SPSS packages.

* Forward selection -2 Log Likelihood 230.743

Variable	B	S.E.	Wald	Sig
STEM1	-.0345	1.2542	.0008	.9781
STEM2	5.4892	13.5298	.1646	.6850
STEM3	-.5076	.9329	.2960	.5864
LOGRAT	6.0335	2.2225	7.3698	.0066
Constant	-.5907	.9175	.4145	.5197

Backward selection -2 Log Likelihood 213.244

Variable	B	S.E.	Wald	Sig
MLDIAM	.0664	.0214	9.6618	.0019
MLDIST	-.0024	.0010	6.3147	.0120
STEM1	.2503	1.3449	.0346	.8523
STEM2	5.3100	13.5320	.1540	.6948
STEM3	-.2647	.9694	.0746	.7848
LPIEN	-51.2432	19.8802	6.6440	.0099
Constant	-.3377	.9714	.1208	.7281

APPENDIX A. Trapping data.

Table A.1. Frequency count for all small mammals trapped in aspen, conifer and mixed forests in the central Rocky Mountains in 1987 through 1989.

SPECIES	ASPEN	CONIFER	MIXED	TOTAL
Clethrionomys gapperi	1302	1277	407	2986
Microtus longicaudus	113	4	29	146
Microtus montanus	133	10	32	175
Microtus species	8	0	1	9
unknown vole	0	0	3	3
Mustela erminea	4	2	1	7
Mustela frenata	2	1	1	4
Peromyscus maniculatis	1130	56	321	1507
Phenacomys intermedius	3	9	5	17
Sorex cinereus	545	183	126	845
Sorex hoyi	11	6	3	20
Sorex monticolus	431	37	58	526
Sorex palustris	2	2	1	5
Sorex vagrans	2	0	0	2
unknown Sorex	115	16	36	167
Spermophilus lateralis	2	0	0	2
Tamiasciurus hudsonicus	1	0	0	1
Tamias minimus	709	45	68	822
Tamius species	13	1	0	14
Thomomys talpoides	46	10	7	63
Zapus princeps	67	10	12	89

APPENDIX B. Vegetation sampling protocol and summary variables

APPENDIX B.1. Sampling protocol

Variable	Protocol
1. Percent canopy closure.	Read with densimeter at center of 3.0 m^2 plot.
2. Number of woody stems and species composition.	Direct count in 3.0 m^2 plot.
3. Shrub cover and species composition.	Read with 6 m line intercept along outside edge of 3.0 m^2 transect.
4. Shrub and forb profile.	Number of stems and horizontal cover read at 2 heights (0.5 and 1.5 m) in 0.25 m^2 quadrate at 3 locations within the 3.0 m^2 plot (1 center-oriented, 2 randomly located). Cover read with a density board placed 0.5 m from observer (opposite side of plot).
5. Overstory tree size.	Average DBH of nearest overstory tree in four quarters.
6. Overstory tree dispersion.	Average distance of nearest overstory tree in four quarters. This sometimes was greater than 8 m.
7. Understory tree size and dispersion.	Same as 5 and 6 above for understory trees.
8. Herbaceous and graminoid species composition and cover.	Count species and estimate cover in 0.25 m^2 frame at the ground level at center of 3.0 m^2 plot.
9. Overstory tree, and fallen log density.	Average number of trees, and and logs in each quarter to 8 m radius.
10. Soil-litter depth.	Litter depth (cm) to mineral soil, general soil texture in 0.25 m^2 plot.
11. Soil surface exposure.	Estimated percent by cover type in 0.25 m^2 plot at ground level at center of plot.

APPENDIX B.2. Computations for vegetation summary variables

I. INPUT FILE - VEG1.DAT, PROGRAM - SUM1.SAS, OUTPUT - SUM1.DAT

A. Shrub Cover (line intercept)

1. (Centimeters of cover / 600 centimeters) * 100
   a. PCOVER - all species pooled
   b. PCONCOV - conifer shrubs pooled
   c. PDECCOV - mast producing deciduous shrubs pooled

2. (Freq / total freq)*100
   a. PCONFR - conifer shrubs pooled
   b. PMDECFR - mast producing deciduous shrubs pooled
   c. POTHER - other deciduous shrubs
   d. PASPEN - quaken aspen

B. Canopy Closure

1. CCAVE - average canopy closure

C. Ground Cover

1. GRFBS - percent of grass and forb cover (grass + forb)

D. Grass/Sedge Species

1. DOCO - 1=grass dominant, grass co-dominant
   2=grass dominant, sedge co-dominant
   3=sedge dominant, sedge co-dominant
   4=sedge dominant, grass co-dominant

E. Litter Depth

1. AVLITTER - average of left and right litter depth

F. Soil type

1. SOILTYPE - 1=rock
   2=gravel
   3=sand
   4=clay
   5=loam

G. Log Density

1. LOGAREA - log frequency / (pi * 8^2 m)

II. SUM23.DAT (Built from VEG23.DAT)

A. Herb/Shrub Profile

1. MHFQ2 - Σ(herb frequencies)/3 at height 0.5 meters
2. MHFQ3 - Σ(herb frequencies)/3 at height 1.5 meters
3. MSFQ2 - Σ(shrub frequencies)/3 at height 0.5 meters
4. MSFQ3 - Σ(shrub frequencies)/3 at height 1.5 meters
5. SDHFQ2 - st. deviation for herbs at height 0.5 meters
6. SDHFQ3 - st. deviation for herbs at height 1.5 meters
7. SDSFQ2 - st. deviation for shrubs at height 0.5 meters
8. SDSFQ3 - st. deviation for shrubs at height 1.5 meters

APPENDIX B.2 cont'd.

III. SUM4.DAT (Built from VEG4.DAT)

A. Tree size/Dispersion and Log dispersion
   1. Mean diameter
      a. MTDIAM - pooled over all trees
      b. MLDIAM - log
      c. MABLADM - subalpine fir
      d. MPOTRDM - quaken aspen
      e. MPICODM - lodgepole pine
      f. MPIENDM - engelman spruce

   2. Mean Distance
      a. MTDIST - pooled over all trees
      b. MLDIST - log
      c. MABLADST - subalpine fir
      d. MPOTRDST - quaken aspen
      e. MPICODST - lodgepole pine
      f. MPIENDST - engelman spruce

   3. Σ(diameter) / Σ(distance)
      a. TREERAT - pooled over all trees
      b. LOGRAT - log
      c. ABLARAT - subalpine fir
      d. POTRRAT - quaken aspen
      e. PICORAT - lodgepole pine
      f. PIENRAT - engelman spruce

   4. Live/dead stems
      a. LIVEDEAD 1=all stems measured are live
                  2=all stems measured are dead
                  3=measured live and dead stems
                  4=variable not recorded

B. Tree Species/Density
   1. Stem type
      a. STEMTYPE 0=no stems present
                  1=all aspen
                  2=all conifer
                  3=all other deciduous
                  4=mixed

   2. Stem frequency / area searched
      a. LIVEAREA - live stems
      b. DEADAREA - dead stems
      c. LABLA - live subalpine fir
      d. DABLA - dead subalpine fir
      e. LPOTR - live aspen
      f. DPOTR - dead aspen
      g. LPICO - live lodgepole pine
      h. DPICO - dead lodgepole pine
      i. LPIEN - live engelman spruce
      j. DPIEN - dead engelman spruce

APPENDIX B.2 cont'd.

IV. QU.DAT (Built from veg4.dat using Quarter circle sampling method)

A. Stem density in hectares

$$\frac{4n - E' - 1}{(\pi/4) * \Sigma(d_{i2})}$$

n - number of stems
E' - number of empty quarter circles and number of quarter circles with other species
d_i - distance to nearest stem or radious when empty

1. TDEN - pooled over all trees
2. ABLADEN - subalpine fir
3. POTRDEN - quaken aspen
4. PICODEN - lodgepole pine
5. PIENDEN - engelman spruce

Appendix C. Chi-square goodness of fit test.

Table C.1. Chi-square goodness of fit test with nine cells and eight degrees of freedom to test for spatial coverage on each plot in the south region.

PLOT	P-VALUE
SA1	0.8789
SA2	0.8229
SA3	0.8505
SA4	0.9947
SA5	0.3840
SA6	0.8793
SA7	0.5809
SA8	0.8479
SA9	0.3657
SC1	0.1234
SC2	0.8535
SC3	0.7850
SM1	0.9161
SM2	0.6122
SM3	0.2168

APPENDIX D. Minimum sufficient statistics.

Table D.1. Minimum sufficient statistics for the M_{bh} model in program CAPTURE stratified by habitat and pooled over year and region.

	TRAP NIGHT					
	1	2	3	4	5	6
Clethrionomys gapperi						
ASPEN	240	283	221	199	170	189
CONIFER	213	228	234	251	197	154
MIXED	73	77	83	70	58	46
Peromyscus maniculatis						
ASPEN	293	249	203	162	115	108
CONIFER	10	9	9	9	12	7
MIXED	74	72	58	41	36	40
Sorex cinereus						
ASPEN	83	94	100	81	102	85
CONIFER	17	24	25	37	46	34
MIXED	22	17	23	22	30	12
Sorex monticolus						
ASPEN	55	53	76	92	81	74
CONIFER	4	5	5	11	6	6
MIXED	4	8	17	9	10	10
Tamius minimus						
ASPEN	142	180	145	109	77	56
CONIFER	11	9	16	4	1	4
MIXED	16	11	13	11	9	8

APPENDIX E. Boundary strip estimates

Table E.1. Average maximum distance between trapping points for eight species stratified by habitat and pooled over region and year.

	ASPEN	CONIFER	MIXED	POOLED MEAN
Clethrionomys gapperi	36.645	40.905	34.545	38.055
Microtus longicaudus	23.790	0.000	18.540	22.800
Microtus montanus	29.130	55.530	11.250	28.305
Peromyscus maniculatis	38.970	43.515	45.765	40.635
Sorex cinereus	77.850	46.170	0.000	63.765
Sorex monticolus	28.215	0.000	15.000	25.995
Tamius minimus	52.500	61.935	56.160	53.460
Zapus princeps	60.585	60.000	54.600	59.385

APPENDIX F. Repeated measures analysis of variance (RMANOVA) output for small mammals trapped in the central Rocky Mountains, 1987-1989. Included for each small mammal is the RMANOVA table, table of least square means, and graphs of main effects and interactions. Output is arranged in alphabetical order by scientific names of each species.

Table F.3. Repeated measures analysis of variance table for Microtus montanus abundances in aspen, conifer and mixed tree types in two regions for the years 1987-1989.

SOURCE	DF	TYPE III SS	MS	F	Pr > F	HF Adj Pr > F
REG	1	24.54	24.54	1.58	0.22	
HAB	2	81.09	40.54	2.62	0.09	
REG*HAB	2	16.62	8.31	0.54	0.59	
ERROR(PLOT)	24	372.01	15.50			
YEAR	2	46.44	23.22	2.01		0.15
YEAR*REG	2	67.85	33.92	2.94		0.06
YEAR*HAB	4	28.15	7.04	0.61		0.65
YEAR*REG*HAB	4	52.65	13.16	1.14		0.35
ERROR(YEAR)	48	554.06	11.54			

Huynh-Feldt Epsilon = 0.9834

Table F.4. Least square means for Microtus montanus abundances.

	1987	1988	1989
NORTH ASPEN	0.14	2.58	5.29
NORTH CONIFER	0.00	1.33	0.00
NORTH MIXED	0.44	0.00	2.67
SOUTH ASPEN	2.03	5.83	2.17
SOUTH CONIFER	0.67	0.67	0.67
SOUTH MIXED	2.67	7.56	0.89

	1987	1988	1989
ASPEN	1.08	4.20	3.73
CONIFER	0.33	1.00	0.33
MIXED	1.56	3.78	1.78

	1987	1988	1989
NORTH	0.19	1.30	2.65
SOUTH	1.79	4.68	1.24

	1987	1988	1989
MARGINAL MEAN	0.99	2.99	1.95

	ASPEN	CONIFER	MIXED
NORTH	2.67	0.44	1.04
SOUTH	3.35	0.67	3.70

	ASPEN	CONIFER	MIXED
MARGINAL MEAN	3.01	0.56	2.37

	NORTH	SOUTH
MARGINAL MEAN	1.38	2.57

GRAND MEAN	1.98

* significant at .05 level
** significant at .01 level
*** significant at .001 level

Table F.3. Repeated measures analysis of variance table for Peromyscus maniculatis abundances in aspen, conifer and mixed tree types in two regions for the years 1987-1989.

SOURCE	DF	TYPE III SS	MS	F	Pr > F	HF Adj Pr > F
REG	1	2108.05	2108.05	5.44	0.03	
HAB	2	8315.28	4157.64	10.73	0.00	
REG*HAB	2	2365.45	1182.72	3.05	0.07	
ERROR(PLOT)	24	9296.76	387.36			
YEAR	2	2940.17	1470.09	7.90		0.00
YEAR*REG	2	4523.12	2261.56	12.15		0.00
YEAR*HAB	4	561.63	140.41	0.75		0.56
YEAR*REG*HAB	4	1970.16	492.54	2.65		0.04
ERROR(YEAR)	48	8935.38	186.15			

Huynh-Feldt Epsilon = 1.2985

Table F.4. Least square means for Peromyscus maniculatis abundances.

*	1987	1988	1989
NORTH ASPEN	6.29	2.92	40.37
NORTH CONIFER	0.51	0.51	11.28
NORTH MIXED	14.39	5.33	55.42
SOUTH ASPEN	45.59	48.05	30.24
SOUTH CONIFER	2.56	2.56	11.28
SOUTH MIXED	35.17	30.38	30.38

	1987	1988	1989
ASPEN	25.94	25.48	35.31
CONIFER	1.54	1.54	11.28
MIXED	24.78	17.85	42.90

**	1987	1988	1989
NORTH	7.07	2.92	35.69
SOUTH	27.78	27.00	23.96

***	1987	1988	1989
MARGINAL MEAN	17.42	14.96	29.83

	ASPEN	CONIFER	MIXED
NORTH	16.53	4.10	25.05
SOUTH	41.30	5.47	31.97

***	ASPEN	CONIFER	MIXED
MARGINAL MEAN	28.91	4.78	28.51

*	NORTH	SOUTH
MARGINAL MEAN	15.23	26.25

GRAND MEAN	20.74

* significant at .05 level
** significant at .01 level
*** significant at .001 level

Table F.5. Repeated measures analysis of variance table for Sorex cinereus abundances in aspen, conifer and mixed tree types in two regions for the years 1987-1989.

SOURCE	DF	TYPE III SS	MS	F	Pr > F	HF Adj Pr > F
REG	1	14697.84	14697.84	6.32	0.02	
HAB	2	45397.58	22698.79	9.76	0.00	
REG*HAB	2	67883.19	33941.59	14.60	0.00	
ERROR(PLOT)	24	55789.66	2324.57			
YEAR	2	21247.55	10623.78	10.13		0.00
YEAR*REG	2	5029.40	2514.70	2.40		0.11
YEAR*HAB	4	9025.08	2256.27	2.15		0.09
YEAR*REG*HAB	4	13925.92	3481.48	3.32		0.02
ERROR(YEAR)	48	50328.06	1048.50			

Huynh-Feldt Epsilon = 0.9328

Table F.6. Least square means for Sorex cinereus abundances.

*	1987	1988	1989
NORTH ASPEN	17.51	9.48	19.69
NORTH CONIFER	76.98	20.88	65.24
NORTH MIXED	1.84	1.38	3.23
SOUTH ASPEN	172.87	45.22	132.75
SOUTH CONIFER	49.58	3.91	22.18
SOUTH MIXED	27.19	11.52	12.90

	1987	1988	1989
ASPEN	95.19	27.35	76.22
CONIFER	63.28	12.40	43.71
MIXED	14.51	6.45	8.06

	1987	1988	1989
NORTH	32.11	10.58	29.39
SOUTH	83.21	20.22	55.94

***	1987	1988	1989
MARGINAL MEAN	57.66	15.40	42.67

***	ASPEN	CONIFER	MIXED
NORTH	15.56	54.37	2.15
SOUTH	116.95	25.23	17.20

***	ASPEN	CONIFER	MIXED
MARGINAL MEAN	66.25	39.80	9.68

*	NORTH	SOUTH
MARGINAL MEAN	24.03	53.13

GRAND MEAN	38.58

* significant at .05 level
** significant at .01 level
*** significant at .001 level

Table F.7. Repeated measures analysis of variance table for Sorex monticolus abundances in aspen, conifer and mixed tree types in two regions for the years 1987-1989.

SOURCE	DF	TYPE III SS	MS	F	Pr > F	HF Adj Pr > F
REG	1	973.42	973.42	5.23	0.03	
HAB	2	4757.28	2378.64	12.79	0.00	
REG*HAB	2	920.60	460.30	2.48	0.11	
ERROR(PLOT)	24	4462.97	185.96			
YEAR	2	1038.70	519.35	5.63		0.01
YEAR*REG	2	181.61	90.81	0.98		0.38
YEAR*HAB	4	1068.55	267.14	2.90		0.03
YEAR*REG*HAB	4	209.37	52.34	0.57		0.69
ERROR(YEAR)	48	4427.26	92.23			

Huynh-Feldt Epsilon = 1.1144

Table F.8. Least square means for Sorex monticolus abundances.

	1987	1988	1989
NORTH ASPEN	12.39	4.13	16.01
NORTH CONIFER	5.27	1.22	2.03
NORTH MIXED	1.06	0.00	2.64
SOUTH ASPEN	27.62	11.10	40.02
SOUTH CONIFER	3.65	0.00	2.84
SOUTH MIXED	12.66	3.69	10.55

*	1987	1988	1989
ASPEN	20.01	7.62	28.01
CONIFER	4.46	0.61	2.43
MIXED	6.86	1.85	6.59

	1987	1988	1989
NORTH	6.24	1.78	6.89
SOUTH	14.65	4.93	17.80

**	1987	1988	1989
MARGINAL MEAN	10.44	3.36	12.35

	ASPEN	CONIFER	MIXED
NORTH	10.84	2.84	1.23
SOUTH	26.25	2.16	8.97

***	ASPEN	CONIFER	MIXED
MARGINAL MEAN	18.55	2.50	5.10

*	NORTH	SOUTH
MARGINAL MEAN	4.97	12.46

GRAND MEAN	8.72

* significant at .05 level
** significant at .01 level
*** significant at .001 level

Table F.9. Repeated measures analysis of variance table for Tamias minimus abundances in aspen, conifer and mixed tree types in two regions for the years 1987-1989.

SOURCE	DF	TYPE III SS	MS	F	Pr > F	HF Adj Pr > F
REG	1	282.96	282.96	1.44	0.24	
HAB	2	3044.32	1522.16	7.74	0.00	
REG*HAB	2	114.77	57.39	0.29	0.75	
ERROR(PLOT)	24	4720.82	196.70			
YEAR	2	388.65	194.32	2.18		0.12
YEAR*REG	2	331.32	165.66	1.86		0.17
YEAR*HAB	4	536.45	134.11	1.51		0.22
YEAR*REG*HAB	4	556.77	139.19	1.56		0.20
ERROR(YEAR)	48	4274.99	89.06			

Huynh-Feldt Epsilon = 1.2650

Table F.10. Least square means for Tamias minimus abundances.

	1987	1988	1989
NORTH ASPEN	9.66	9.39	28.16
NORTH CONIFER	0.00	0.73	1.09
NORTH MIXED	0.59	0.59	8.88
SOUTH ASPEN	24.02	9.39	17.26
SOUTH CONIFER	4.01	4.01	6.57
SOUTH MIXED	8.28	13.02	8.8

	1987	1988	1989
ASPEN	16.84	9.39	22.71
CONIFER	2.01	2.37	3.83
MIXED	4.44	6.80	8.88

	1987	1988	1989
NORTH	3.42	3.57	12.71
SOUTH	12.11	8.81	10.90

	1987	1988	1989
MARGINAL MEAN	7.76	6.19	11.81

	ASPEN	CONIFER	MIXED
NORTH	15.74	0.61	3.35
SOUTH	16.89	4.86	10.06

**	ASPEN	CONIFER	MIXED
MARGINAL MEAN	16.31	2.74	6.71

	NORTH	SOUTH
MARGINAL MEAN	6.57	10.60

GRAND MEAN	8.59

* significant at .05 level
** significant at .01 level
*** significant at .001 level

Table F.11. Repeated measures analysis of variance table for Zapus princeps abundances in aspen, conifer and mixed tree types in two regions for the years 1987-1989.

SOURCE	DF	TYPE III SS	MS	F	Pr > F	HF Adj Pr > F
REG	1	36.97	36.97	3.20	0.09	
HAB	2	30.18	15.09	1.31	0.29	
REG*HAB	2	14.69	7.34	0.64	0.54	
ERROR(PLOT)	24	277.16	11.55			
YEAR	2	19.97	9.98	0.76		0.47
YEAR*REG	2	27.90	13.95	1.06		0.35
YEAR*HAB	4	20.56	5.14	0.39		0.80
YEAR*REG*HAB	4	31.40	7.85	0.60		0.66
ERROR(YEAR)	48	633.04	13.19			

Huynh-Feldt Epsilon = 0.9243

Table F.12. Least square means for Zapus princeps abundances.

	1987	1988	1989
NORTH ASPEN	0.00	0.32	1.30
NORTH CONIFER	0.67	0.00	0.00
NORTH MIXED	0.00	0.35	0.00
SOUTH ASPEN	5.18	3.72	0.32
SOUTH CONIFER	2.67	0.00	0.00
SOUTH MIXED	0.35	3.52	0.00

	1987	1988	1989
ASPEN	2.59	2.02	0.81
CONIFER	1.67	0.00	0.00
MIXED	0.18	1.94	0.00

	1987	1988	1989
NORTH	0.22	0.23	0.43
SOUTH	2.73	2.42	0.11

	1987	1988	1989
MARGINAL MEAN	1.48	1.32	0.27

	ASPEN	CONIFER	MIXED
NORTH	0.54	0.22	0.12
SOUTH	3.08	0.89	1.29

	ASPEN	CONIFER	MIXED
MARGINAL MEAN	1.81	0.56	0.70

	NORTH	SOUTH
MARGINAL MEAN	0.29	1.75

GRAND MEAN	1.02

* significant at .05 level
** significant at .01 level
*** significant at .001 level

Table F.13. Repeated measures analysis of variance table for Microtus longicaudus abundances in aspen, conifer and mixed tree types in two regions for the years 1987-1989.

SOURCE	DF	TYPE III SS	MS	F	Pr > F	HF Adj Pr > F
REG	1	72.54	72.54	1.92	0.18	
HAB	2	78.97	39.49	1.05	0.37	
REG*HAB	2	25.35	12.68	0.34	0.72	
ERROR(PLOT)	24	905.45	37.73			
YEAR	2	135.10	67.55	1.91		0.17
YEAR*REG	2	176.47	88.23	2.49		0.11
YEAR*HAB	4	41.22	10.31	0.29		0.83
YEAR*REG*HAB	4	103.30	25.83	0.73		0.54
ERROR(YEAR)	48	1702.01	35.46			

Huynh-Feldt Epsilon = 0.7406

Table F.14. Least square means for Microtus longicaudus abundances.

	1987	1988	1989
NORTH ASPEN	0.00	0.29	4.42
NORTH CONIFER	0.00	0.43	0.00
NORTH MIXED	0.00	0.00	0.00
SOUTH ASPEN	0.71	9.99	0.71
SOUTH CONIFER	0.00	1.28	0.00
SOUTH MIXED	0.37	8.97	1.49

	1987	1988	1989
ASPEN	0.36	5.14	2.57
CONIFER	0.00	0.86	0.00
MIXED	0.19	4.48	0.75

	1987	1988	1989
NORTH	0.00	0.24	1.47
SOUTH	0.36	6.75	0.74

	1987	1988	1989
MARGINAL MEAN	0.18	3.49	1.11

	ASPEN	CONIFER	MIXED
NORTH	1.57	0.14	0.00
SOUTH	3.80	0.43	3.61

	ASPEN	CONIFER	MIXED
MARGINAL MEAN	2.69	0.29	1.81

	NORTH	SOUTH
MARGINAL MEAN	0.57	2.61

GRAND MEAN	1.59

* significant at .05 level
*** significant at .001 level

APPENDIX G
Habitat selection function models for five species.

CODING FOR DESIGN VARIABLES

Table G.1. Design variables for dominance and codominance of grass and sedge species, types of trees present at each point, and type of soil at each point. These variables were included in the logistic regression procedure to build habitat selection functions for eight species in each habitat and region.

DOCO	GG
1-grass/grass	1
2-grass/sedge	1
3-sedge/sedge	0
4-sedge/grass	0

STEMTYPE	STEM1	STEM2	STEM3	STEM4
1- aspen	0	0	0	0
2- conifer	1	0	0	0
3- deciduous	0	1	0	0
4- mixed	0	0	1	0
0- no stems	0	0	0	1

SOILTYPE	SOIL1	SOIL2	SOIL3	SOIL4
5- rock	0	0	0	0
4- gravel	1	0	0	0
3- sand	0	1	0	0
2- clay	0	0	1	0
1- loam	0	0	0	1

Table G.2. Variables removed from the set of variables considered in the logistic regression forward and backward selection procedures due to assumed high correlation. These variables had high variance inflation factors in PROC REG of SAS packages when included in a multiple regression model with all of the other variables in the vegetation data set.

ORDER REMOVED	VARIABLE
1	PCOVER
2	SOILTYPE
3	DEADAREA
4	LIVEAREA

Table G.3. Estimated habitat selection functions for Microtus montanus in the Aspen habitat and north region built with logistic regression forward and backward selection routines in SPSS packages.

Forward Selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		551.990			
1	IN: STEM1	531.935	20.055	1	.000

Forward Selection model -2 Log Likelihood 665.404

Variable	B	S.E.	Wald	Sig
STEM1	-2.3398	.7238	10.4506	.0012
STEM2	2.2101	1.2347	3.2039	.0735
STEM3	-.4035	.2346	2.9586	.0854
STEM4	1.8046	1.1653	2.3983	.1215
Constant	-2.9032	.1566	343.5861	.0000

Backward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		468.293			
2	OUT: MSFQ3	468.293	0.000	1	.989
3	OUT: STEM4	468.727	-0.434	1	.510
4	OUT: STEM3	468.746	-0.019	1	.891
5	OUT: POTHCOV	470.082	-1.336	1	.248
6	OUT: DPIEN	470.791	-0.709	1	.400
7	OUT: LPIEN	470.794	-0.003	1	.960
8	OUT: STEM1	475.650	-4.856	1	.028
9	OUT: MSFQ2	475.864	-0.214	1	.643
10	OUT: DPICO	479.760	-3.896	1	.048
11	OUT: MTDIST	480.044	-0.284	1	.594
12	OUT: DPOTR	480.359	-0.315	1	.575
13	OUT: LPICO	480.983	-0.624	1	.430
14	OUT: PCONCOV	483.331	-2.348	1	.125
15	OUT: STEM2	483.891	-0.560	1	.454

Backward selection model -2 Log Likelihood 508.185

Variable	B	S.E.	Wald	Sig
GG	.5868	.3387	3.0010	.0832
AVLITTER	-.2343	.1070	4.7973	.0285
LOGAREA	-9.4308	4.3023	4.8051	.0284
MHFQ2	.0497	.0228	4.7486	.0293
MLDIST	-.0016	.0006	7.6224	.0058
LABLA	-52.0416	18.3787	8.0181	.0046
Constant	-2.2483	.4426	25.8003	.0000

Table G.4. Estimated habitat selection functions for Peromyscus maniculatis in the aspen habitat and north region built with logistic regression forward and backward selection routines in SPSS packages.

Forward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		880.816			
1	IN: MLDIST	804.458	76.358	1	.000
2	IN: STEM3	786.610	17.848	1	.000
3	IN: MHFQ2	760.306	26.304	1	.000
4	IN: CCAVE	752.537	7.769	1	.005
5	IN: AVLITTER	746.868	5.669	1	.017
6	IN: MSFQ3	741.904	4.964	1	.026

Forward selection model -2 Log Likelihood 742.928

Variable	B	S.E.	Wald	Sig
MLDIST	-.0025	.0004	34.9419	.0000
STEM3	.5365	.1916	7.8424	.0051
STEM4	.1868	22.2521	.0001	.9933
MHFQ2	-.1593	.0396	16.1498	.0001
CCAVE	.0144	.0048	9.0699	.0026
AVLITTER	-.1821	.0716	6.4715	.0110
MSFQ3	.3067	.1312	5.4621	.0194
Constant	-.3277	.3743	.7666	.3813

Backward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		715.722			
2	OUT: STEM4	715.725	-0.003	1	.959
3	OUT: GG	715.741	-0.016	1	.900
4	OUT: LABLA	715.776	-0.035	1	.852
5	OUT: MTDIAM	715.897	-0.121	1	.728
6	OUT: LOGAREA	716.041	-0.144	1	.705
7	OUT: POTHCOV	718.853	-2.812	1	.094
8	OUT: LPOTR	719.117	-0.264	1	.607
9	OUT: MTDIST	719.532	-0.415	1	.520
10	OUT: TREERAT	719.590	-0.058	1	.809
11	OUT: MHFQ3	720.079	-0.489	1	.484
12	OUT: LOGRAT	722.580	-2.501	1	.114
13	OUT: PCONCOV	723.612	-1.032	1	.310
14	OUT: PPOTRCV	724.888	-1.276	1	.259
15	OUT: MSFQ2	730.388	-5.500	1	.019
16	OUT: PDECCOV	732.588	-2.200	1	.138
17	OUT: GRFBS	734.866	-2.278	1	.131

Backward selection model -2 Log Likelihood 736.082

Variable	B	S.E.	Wald	Sig
CCAVE	.0136	.0048	7.9351	.0048
AVLITTER	-.1813	.0719	6.3637	.0116
MHFQ2	-.1636	.0396	17.0570	.0000
MSFQ3	.3354	.1357	6.1077	.0135
MLDIAM	-.0478	.0239	4.0180	.0450
MLDIST	-.0025	.0004	33.3712	.0000
STEM3	.4981	.1933	6.6413	.0100
STEM4	-.0531	22.2525	.0000	.9981
DPOTR	-9.0473	4.5151	4.0151	.0451
Constant	.6737	.5712	1.3912	.2382

Table G.5. Estimated habitat selection functions for Peromyscus maniculatis in the conifer habitat and north region built with logistic regression forward and backward selection routines is SPSS packages.

Forward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		144.680			
1	IN: STEM1	140.488	4.192	1	.041

Forward selection model -2 Log Likelihood 156.044

Variable	B	S.E.	Wald	Sig
STEM1	-8.3969	22.2406	.1425	.7058
Constant	6.1997	22.2395	.0777	.7804

Backward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		111.628			
2	OUT: MSFQ2	111.631	-0.003	1	.959
3	OUT: MTDIAM	111.634	-0.003	1	.958
4	OUT: PCONCOV	111.640	-0.006	1	.939
5	OUT: MLDIAM	111.646	-0.006	1	.936
6	OUT: DPICO	111.659	-0.013	1	.911
7	OUT: MSFQ3	111.684	-0.025	1	.874
8	OUT: POTHCOV	112.259	-0.575	1	.448
9	OUT: STEM1	118.693	-6.434	1	.011
10	OUT: MHFQ2	118.820	-0.127	1	.721
11	OUT: PDECCOV	119.166	-0.346	1	.557
12	OUT: LABLA	119.778	-0.612	1	.434
13	OUT: MTDIST	120.333	-0.555	1	.456
14	OUT: LOGRAT	120.986	-0.653	1	.419
15	OUT: MLDIST	121.389	-0.403	1	.526
16	OUT: MHFQ3	122.369	-0.980	1	.322
17	OUT: DPIEN	122.883	-0.514	1	.473
18	OUT: GRFBS	123.719	-0.836	1	.361
19	OUT: DABLA	125.411	-1.692	1	.193
20	OUT: LPICO	126.548	-1.137	1	.286
21	OUT: AVLITTER	129.060	-2.512	1	.113

Backward selection model -2 Log Likelihood 145.631

Variable	B	S.E.	Wald	Sig
CCAVE	.0432	.0150	8.2863	.0040
LOGAREA	-7.3369	6.7747	1.1729	.2788
TREERAT	-13.2511	8.7255	2.3064	.1288
STEM1	-9.4321	22.2575	.1796	.6717
Constant	5.9657	22.2404	.0720	.7885

Table G.6. Estimated habitat selection functions for Peromyscus maniculatis in the mixed habitat and north region built with logistic regression forward and backward selection routines in SPSS packages.

Forward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		239.777			
1	IN: GRFBS	222.111	17.666	1	.000
2	IN: AVLITTER	211.282	10.829	1	.001
3	IN: MLDIST	195.467	15.815	1	.000
4	IN: POTHCOV	190.344	5.123	1	.024

Forward selection model -2 Log Likelihood 249.023

Variable	B	S.E.	Wald	Sig
GRFBS	-.0207	.0071	8.4315	.0037
AVLITTER	-.2819	.0841	11.2431	.0008
MLDIST	-.0020	.0005	17.6545	.0000
POTHCOV	.9403	.5045	3.4739	.0623
Constant	1.9647	.3892	25.4820	.0000

Backward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		153.027			
2	OUT: STEM1	153.027	0.000	1	.987
3	OUT: DPOTR	153.036	-0.009	1	.924
4	OUT: MTDIST	153.044	-0.008	1	.927
5	OUT: MLDIAM	153.078	-0.034	1	.854
6	OUT: MSFQ2	153.117	-0.039	1	.843
7	OUT: MTDIAM	153.195	-0.078	1	.780
8	OUT: PPOTRCV	153.312	-0.117	1	.733
9	OUT: STEM3	155.135	-1.823	1	.177
10	OUT: POTHCOV	159.917	-4.782	1	.029
11	OUT: PDECCOV	160.276	-0.359	1	.549
12	OUT: LOGRAT	160.797	-0.521	1	.471
13	OUT: DABLA	161.482	-0.685	1	.408
14	OUT: GG	162.555	-1.073	1	.300
15	OUT: PCONCOV	163.839	-1.284	1	.257
16	OUT: LPOTR	164.910	-1.071	1	.301
17	OUT: DPICO	166.074	-1.164	1	.281
18	OUT: LOGAREA	167.956	-1.882	1	.170
19	OUT: MHFQ3	170.669	-2.713	1	.100

Backward selection model -2 Log Likelihood 170.815

Variable	B	S.E.	Wald	Sig
POTHCOV	.9839	.9675	1.0343	.3092
CCAVE	.0174	.0121	2.0773	.1495
GRFBS	-.0246	.0089	7.5952	.0059
AVLITTER	-.2505	.1261	3.9454	.0470
MHFQ2	-.2681	.1541	3.0257	.0820
MLDIST	-.0017	.0005	9.7099	.0018
TREERAT	-9.9430	5.9947	2.7511	.0972
LABLA	-7.5819	4.6752	2.6300	.1049
LPICO	-11.0140	3.7914	8.4389	.0037
Constant	2.9866	1.1072	7.2763	.0070

Table G.7. Estimated habitat selection functions for Peromyscus maniculatis in the aspen habitat and south region built with logistic regression forward and backward selection routines in SPSS packages.

Forward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		654.409			
1	IN: LOGAREA	648.577	5.832	1	.016
2	IN: CCAVE	644.059	4.518	1	.034

Forward selection model -2 Log Likelihood 700.169

Variable	B	S.E.	Wald	Sig
LOGAREA	7.8174	3.0762	6.4579	.0110
CCAVE	.0142	.0066	4.5395	.0331
Constant	-1.8442	.5793	10.1363	.0015

Backward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		619.101			
2	OUT: GG	619.108	-0.007	1	.934
3	OUT: LABLA	619.119	-0.011	1	.918
4	OUT: TREERAT	619.150	-0.031	1	.861
5	OUT: PDECCOV	619.190	-0.040	1	.842
6	OUT: MSFQ3	619.258	-0.068	1	.794
7	OUT: STEM4	619.625	-0.367	1	.545
8	OUT: MHFQ2	619.724	-0.099	1	.753
9	OUT: STEM2	620.293	-0.569	1	.450
10	OUT: GRFBS	620.723	-0.430	1	.512
11	OUT: STEM3	621.377	-0.654	1	.419
12	OUT: LPIEN	621.937	-0.560	1	.454
13	OUT: MHFQ3	622.503	-0.566	1	.452
14	OUT: PCONCOV	623.650	-1.147	1	.284
15	OUT: MTDIAM	624.651	-1.001	1	.317
16	OUT: AVLITTER	625.782	-1.131	1	.288
17	OUT: LOGAREA	626.985	-1.203	1	.273
18	OUT: LPOTR	628.389	-1.404	1	.236
19	OUT: MSFQ2	629.903	-1.514	1	.218
20	OUT: LOGRAT	631.939	-2.036	1	.154

Backward selection model -2 Log Likelihood 677.176

Variable	B	S.E.	Wald	Sig
CCAVE	.0174	.0070	6.1383	.0132
MLDIAM	.0422	.0173	5.9158	.0150
DPOTR	-6.4467	2.7146	5.6398	.0176
Constant	-2.0377	.6281	10.5232	.0012

Table G.8. Estimated habitat selection functions for Peromyscus maniculatis in the conifer habitat and south region built with logistic regression forward and backward selection routines in SPSS packages.

Forward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		61.427			
1	IN: POTHCOV	56.409	5.018	1	.025

Forward selection model -2 Log Likelihood 134.385

Variable	B	S.E.	Wald	Sig
POTHCOV	-.5269	1.5206	.1201	.7290
Constant	-2.4879	.2400	107.4644	.0000

Backward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		35.961			
2	OUT: POTHCOV	45.435	-9.474	1	.002
3	OUT: PCONCOV	45.447	-0.012	1	.911
4	OUT: MTDIAM	45.456	-0.009	1	.925
5	OUT: DPOTR	45.466	-0.010	1	.921
6	OUT: MSFQ3	46.172	-0.706	1	.401
7	OUT: TREERAT	46.173	-0.001	1	.975
8	OUT: LOGAREA	46.186	-0.013	1	.910
9	OUT: MLDIAM	46.270	-0.084	1	.773
10	OUT: DPIEN	46.383	-0.113	1	.736
11	OUT: LPOTR	46.528	-0.145	1	.703
12	OUT: PDECCOV	46.656	-0.128	1	.721
13	OUT: DABLA	46.860	-0.204	1	.652
14	OUT: AVLITTER	47.149	-0.289	1	.591
15	OUT: GG	47.405	-0.256	1	.613
16	OUT: STEM1	48.363	-0.958	1	.328
17	OUT: LABLA	49.219	-0.856	1	.355
18	OUT: MHFQ2	50.119	-0.900	1	.343
19	OUT: GRFBS	51.175	-1.056	1	.304
20	OUT: MLDIST	52.420	-1.245	1	.264
21	OUT: MHFQ3	53.391	-0.971	1	.324
22	OUT: CCAVE	55.518	-2.127	1	.145

Backward selection model -2 Log Likelihood 133.903

Variable	B	S.E.	Wald	Sig
LOGRAT	.7553	.9432	.6411	.4233
Constant	-2.6148	.2876	82.6418	.0000

Table G.9. Estimated habitat selection functions for Peromyscus maniculatis in the mixed habitat and south region built with logistic regression forward and backward selection routines in SPSS packages.

Forward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		178.079			
1	IN: MLDIAM	172.217	5.862	1	.015
2	IN: DPOTR	166.231	5.986	1	.014

Forward selection model -2 Log Likelihood 237.492

Variable	B	S.E.	Wald	Sig
MLDIAM	-.0341	.0196	3.0159	.0825
DPOTR	-15.8086	8.5883	3.3882	.0657
Constant	.1079	.3442	.0983	.7538

Backward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		137.686			
2	OUT: MTDIST	137.686	0.000	1	.987
3	OUT: GG	137.687	-0.001	1	.970
4	OUT: STEM2	138.339	-0.652	1	.419
5	OUT: MSFQ2	138.340	-0.001	1	.981
6	OUT: MTDIAM	138.347	-0.007	1	.933
7	OUT: PCONCOV	138.364	-0.017	1	.897
8	OUT: STEM3	138.406	-0.042	1	.837
9	OUT: MHFQ2	138.485	-0.079	1	.779
10	OUT: MSFQ3	141.601	-3.116	1	.078
11	OUT: LABLA	141.960	-0.359	1	.549
12	OUT: PDECCOV	142.443	-0.483	1	.487
13	OUT: LPIEN	143.274	-0.831	1	.362
14	OUT: DABLA	144.197	-0.923	1	.337
15	OUT: STEM1	144.789	-0.592	1	.442
16	OUT: LPOTR	146.121	-1.332	1	.248
17	OUT: CCAVE	147.217	-1.096	1	.295
18	OUT: TREERAT	148.361	-1.144	1	.285

Backward selection model -2 Log Likelihood 231.577

Variable	B	S.E.	Wald	Sig
PPOTRCV	.3075	.2619	1.3789	.2403
GRFBS	-.0120	.0080	2.2322	.1352
MLDIAM	-.0629	.0310	4.1120	.0426
MLDIST	.0003	.0011	.0565	.8121
LOGRAT	3.4316	3.1215	1.2085	.2716
DPOTR	-13.6636	9.0119	2.2988	.1295
Constant	.3918	.4546	.7431	.3887

Table G.10. Estimated habitat selection functions for Sorex cinereus in the aspen habitat and north region built with logistic regression forward and backward selection routines in SPSS packages.

Forward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		228.175			
1	IN: MSFQ2	224.022	4.153	1	.042
2	IN: STEM3	217.731	6.291	1	.012

Forward selection model -2 Log Likelihood 218.328

Variable	B	S.E.	Wald	Sig
MSFQ2	.5715	.2483	5.2959	.0214
STEM3	-1.2298	.5552	4.9063	.0268
STEM4	-4.2356	25.9213	.0267	.8702
Constant	-2.9661	.2175	186.0088	.0000

Backward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		198.854			
2	OUT: LOGRAT	198.854	0.000	1	.993
3	OUT: STEM4	198.872	-0.018	1	.893
4	OUT: GG	198.876	-0.004	1	.951
5	OUT: POTHCOV	199.135	-0.259	1	.611
6	OUT: MHFQ3	199.150	-0.015	1	.901
7	OUT: PPOTRCV	199.168	-0.018	1	.893
8	OUT: GRFBS	199.190	-0.022	1	.883
9	OUT: MTDIST	199.232	-0.042	1	.837
10	OUT: PCONCOV	200.530	-1.298	1	.255
11	OUT: AVLITTER	200.587	-0.057	1	.811
12	OUT: LABLA	200.787	-0.200	1	.655
13	OUT: MTDIAM	200.915	-0.128	1	.721
14	OUT: MLDIAM	201.156	-0.241	1	.623
15	OUT: TREERAT	201.576	-0.420	1	.517
16	OUT: CCAVE	202.078	-0.502	1	.479
17	OUT: PDECCOV	202.862	-0.784	1	.376
18	OUT: DPOTR	204.085	-1.223	1	.269
19	OUT: MHFQ2	204.803	-0.718	1	.397
20	OUT: LOGAREA	206.922	-2.119	1	.145
21	OUT: MLDIST	208.076	-1.154	1	.283
22	OUT: MSFQ3	215.669	-7.593	1	.006
23	OUT: LPOTR	217.730	-2.061	1	.151

Backward selection model -2 Log Likelihood 218.328

Variable	B	S.E.	Wald	Sig
MSFQ2	.5715	.2483	5.2959	.0214
STEM3	-1.2298	.5552	4.9063	.0268
STEM4	-4.2356	25.9213	.0267	.8702
Constant	-2.9661	.2175	186.0088	.0000

Table G.11. Estimated habitat selection functions for Sorex cinereus in the conifer habitat and north region built with logistic regression forward and backward selection routines in SPSS packages.

Forward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		173.000			
1	IN: MLDIAM	167.021	5.979	1	.014

Forward selection model -2 Log Likelihood 209.845

Variable	B	S.E.	Wald	Sig
MLDIAM	-.0588	.0260	5.1116	.0238
Constant	-.4374	.5172	.7153	.3977

Backward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		139.637			
2	OUT: STEM1	139.639	-0.002	1	.968
3	OUT: DPICO	139.639	0.000	1	.983
4	OUT: MSFQ2	140.383	-0.744	1	.388
5	OUT: POTHCOV	142.673	-2.290	1	.130
6	OUT: GRFBS	142.721	-0.048	1	.826
7	OUT: CCAVE	142.759	-0.038	1	.846
8	OUT: MSFQ3	144.187	-1.428	1	.232
9	OUT: DABLA	144.314	-0.127	1	.721
10	OUT: MHFQ2	144.482	-0.168	1	.682
11	OUT: LPICO	144.645	-0.163	1	.686
12	OUT: PDECCOV	144.753	-0.108	1	.743
13	OUT: MHFQ3	144.990	-0.237	1	.627
14	OUT: PCONCOV	145.259	-0.269	1	.604
15	OUT: LOGRAT	145.726	-0.467	1	.494
16	OUT: TREERAT	146.473	-0.747	1	.387
17	OUT: MTDIAM	147.300	-0.827	1	.363
18	OUT: LPIEN	148.358	-1.058	1	.304
19	OUT: GG	149.378	-1.020	1	.313
20	OUT: MLDIAM	150.785	-1.407	1	.236
21	OUT: AVLITTER	151.549	-0.764	1	.382
22	OUT: DPIEN	154.226	-2.677	1	.102

Backward selection model -2 Log Likelihood 207.160

Variable	B	S.E.	Wald	Sig
LOGAREA	-14.0726	6.6341	4.4997	.0339
MTDIST	-.0014	.0012	1.5734	.2097
MLDIST	-.0016	.0010	2.6821	.1015
LABLA	-10.5899	8.0844	1.7159	.1902
Constant	.8040	.8756	.8432	.3585

Note: The intercept was the only significant term in the forward selection procedure, and the backward selection procedure did not converge for Sorex cinereus in the mixed habitat and north region.

Table G.12. Estimated habitat selection functions for Sorex cinereus in the aspen habitat and south region built with logistic regression forward and backward selection routines in SPSS packages.

Forward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		351.100			
1	IN: MLDIAM	347.046	4.054	1	.044

Forward selection model -2 Log Likelihood 370.933

Variable	B	S.E.	Wald	Sig
MLDIAM	-.0479	.0256	3.5130	.0609
Constant	-1.4966	.2921	26.2536	.0000

Backward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		321.087			
2	OUT: STEM4	321.151	-0.064	1	.801
3	OUT: LOGAREA	321.156	-0.005	1	.942
4	OUT: PDECCOV	321.163	-0.007	1	.935
5	OUT: STEM2	322.351	-1.188	1	.276
6	OUT: LPIEN	324.023	-1.672	1	.196
7	OUT: PCONCOV	325.415	-1.392	1	.238
8	OUT: MHFQ2	325.447	-0.032	1	.858
9	OUT: DPOTR	325.478	-0.031	1	.860
10	OUT: MSFQ2	328.351	-2.873	1	.090
11	OUT: POTHCOV	330.424	-2.073	1	.150
12	OUT: STEM3	330.565	-0.141	1	.708
13	OUT: MTDIAM	330.803	-0.238	1	.626
14	OUT: GRFBS	331.116	-0.313	1	.576
15	OUT: GG	331.436	-0.320	1	.571
16	OUT: MHFQ3	331.842	-0.406	1	.524
17	OUT: TREERAT	332.298	-0.456	1	.499
18	OUT: CCAVE	332.843	-0.545	1	.460
19	OUT: MTDIST	333.135	-0.292	1	.589
20	OUT: LOGRAT	333.793	-0.658	1	.417
21	OUT: LABLA	334.685	-0.892	1	.345
22	OUT: AVLITTER	335.627	-0.942	1	.332
23	OUT: PPOTRCV	338.619	-2.992	1	.084
24	OUT: MSFQ3	341.754	-3.135	1	.077
25	OUT: LPOTR	343.719	-1.965	1	.161

Backward selection model -2 Log Likelihood 368.099

Variable	B	S.E.	Wald	Sig
MLDIAM	-.0666	.0294	5.1400	.0234
MLDIST	.0013	.0008	2.9462	.0861
Constant	-1.6301	.3122	27.2670	.0000

Table G.13. Estimated habitat selection functions for Sorex cinereus in the conifer habitat and south region built with logistic regression forward and backward selection routines in SPSS packages. (Note: backward selection did not converge.)

Forward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		40.200			
1	IN: DPIEN	36.206	3.994	1	.046

Forward selection model -2 Log Likelihood 67.145

Variable	B	S.E.	Wald	Sig
DPIEN	43.3553	19.4190	4.9846	.0256
Constant	-3.7578	.4343	74.8509	.0000

Table G.14. Estimated habitat selection functions for Sorex cinereus in the mixed habitat and south region built with logistic regression forward and backward selection routines in SPSS packages.

Forward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		86.700			
1	IN: MLDIST	81.682	5.018	1	.025

Forward selection model -2 Log Likelihood 107.534

Variable	B	S.E.	Wald	Sig
MLDIST	-.0040	.0017	5.2987	.0213
Constant	-1.3568	.4234	10.2665	.0014

Backward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		62.315			
3	OUT: STEM2	62.315	0.000	1	.993
4	OUT: POTHCOV	62.387	-0.072	1	.789
5	OUT: STEM3	64.798	-2.411	1	.120
6	OUT: LABLA	64.799	-0.001	1	.976
7	OUT: GG	64.807	-0.008	1	.927
8	OUT: CCAVE	64.818	-0.011	1	.918
9	OUT: MSFQ2	66.288	-1.470	1	.225
10	OUT: GRFBS	66.303	-0.015	1	.902
11	OUT: MHFQ2	66.342	-0.039	1	.843
12	OUT: MTDIST	66.403	-0.061	1	.805
13	OUT: LPIEN	66.643	-0.240	1	.624
14	OUT: LPOTR	66.960	-0.317	1	.573
15	OUT: MSFQ3	67.247	-0.287	1	.592
16	OUT: PPOTRCV	67.908	-0.661	1	.416
17	OUT: LOGAREA	68.349	-0.441	1	.507
18	OUT: AVLITTER	69.000	-0.651	1	.420
19	OUT: LOGRAT	69.445	-0.445	1	.505
20	OUT: TREERAT	70.045	-0.600	1	.439
21	OUT: PDECCOV	70.779	-0.734	1	.391
22	OUT: DPOTR	71.804	-1.025	1	.311
23	OUT: PCONCOV	73.063	-1.259	1	.262
24	OUT: DPIEN	73.518	-0.455	1	.500
25	OUT: MHFQ3	75.481	-1.963	1	.161
26	OUT: MLDIAM	77.058	-1.577	1	.209
27	OUT: DABLA	80.703	-3.645	1	.056
28	OUT: STEM1	81.724	-1.021	1	.312

Backward selection model -2 Log Likelihood 107.534

Variable	B	S.E.	Wald	Sig
MLDIST	-.0040	.0017	5.2987	.0213
Constant	-1.3568	.4234	10.2665	.0014

Table G.15. Estimated habitat selection functions for Tamius minimus in the aspen habitat and north region built with logistic regression forward and backward selection routines in SPSS packages.

Forward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		858.345			
1	IN: STEM3	835.131	23.214	1	.000
2	IN: MLDIAM	830.476	4.655	1	.031
3	IN: CCAVE	824.047	6.429	1	.011
4	IN: STEM4	820.389	3.658	1	.056

Forward selection model -2 Log Likelihood 840.575

Variable	B	S.E.	Wald	Sig
STEM3	.7340	.1801	16.6109	.0000
STEM4	5.9058	8.2070	.5178	.4718
MLDIAM	.0506	.0189	7.1352	.0076
CCAVE	.0128	.0046	7.9323	.0049
Constant	-2.7221	.4759	32.7128	.0000

Backward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		800.730			
2	OUT: PPOTRCV	800.736	-0.006	1	.940
3	OUT: STEM4	803.432	-2.696	1	.101
4	OUT: AVLITTER	803.462	-0.030	1	.862
5	OUT: LABLA	803.524	-0.062	1	.803
6	OUT: GRFBS	803.596	-0.072	1	.788
7	OUT: LOGAREA	803.707	-0.111	1	.739
8	OUT: PDECCOV	803.856	-0.149	1	.700
9	OUT: POTHCOV	805.835	-1.979	1	.159
10	OUT: PCONCOV	806.027	-0.192	1	.661
11	OUT: MHFQ3	806.419	-0.392	1	.531
12	OUT: DPOTR	806.877	-0.458	1	.498
13	OUT: MLDIST	807.409	-0.532	1	.466
14	OUT: MSFQ2	807.960	-0.551	1	.458
15	OUT: TREERAT	808.673	-0.713	1	.398
16	OUT: MSFQ3	809.867	-1.194	1	.274
17	OUT: MTDIST	810.855	-0.988	1	.320
18	OUT: MTDIAM	811.533	-0.678	1	.410
19	OUT: LPOTR	812.988	-1.455	1	.228
20	OUT: LOGRAT	816.322	-3.334	1	.068
21	OUT: MHFQ2	819.609	-3.287	1	.070
22	IN: STEM4	816.152	3.457	1	.063

Backward selection model -2 Log Likelihood 835.624

Variable	B	S.E.	Wald	Sig
CCAVE	.0119	.0046	6.7829	.0092
GG	.4649	.2135	4.7442	.0294
MLDIAM	.0522	.0190	7.5303	.0061
STEM3	.7646	.1811	17.8325	.0000
STEM4	5.7796	8.2072	.4959	.4813
Constant	-3.0679	.5052	36.8764	.0000

Table G.16. Estimated habitat selection functions for Tamius minimus in the conifer habitat and north region built with logistic regression forward and backward selection routines in SPSS packages. (Note: backward selection did not converge).

Forward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		46.349			
1	IN: LOGAREA	42.036	4.313	1	.038
2	IN: CCAVE	35.832	6.204	1	.013
3	IN: MTDIST	31.700	4.132	1	.042

Forward selection model -2 Log Likelihood 46.394

Variable	B	S.E.	Wald	Sig
LOGAREA	10.7149	8.8388	1.4696	.2254
CCAVE	.0850	.0348	5.9537	.0147
MTDIST	.0049	.0024	4.2400	.0395
Constant	-12.6750	3.6224	12.2434	.0005

Table G.17. Estimated habitat selection functions for Tamius minimus in the mixed habitat and north region built with logistic regression forward and backward selection routines in SPSS packages. (Note: backward selection did not converge).

Forward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		76.425			
1	IN: DABLA	73.609	2.816	1	.093
2	IN: DPICO	56.529	17.080	1	.000

Forward selection model -2 Log Likelihood 66.660

Variable	B	S.E.	Wald	Sig
DABLA	86.0938	54.6882	2.4783	.1154
DPICO	-1748.96	6490.1244	.0726	.7876
Constant	-2.2245	.3382	43.2699	.0000

Table G.18. Estimated habitat selection functions for Tamius minimus in the aspen habitat and south region built with logistic regression forward and backward selection routines in SPSS packages.

Forward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		519.324			
1	IN: LOGAREA	492.611	26.713	1	.000
2	IN: LOGRAT	486.872	5.739	1	.017

Forward selection model -2 Log Likelihood 514.414

Variable	B	S.E.	Wald	Sig
LOGAREA	14.6371	3.8470	14.4764	.0001
LOGRAT	2.8988	1.1306	6.5743	.0103
Constant	-2.0522	.1927	113.3926	.0000

Backward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		466.951			
2	OUT: STEM4	467.131	-0.180	1	.672
3	OUT: GRFBS	467.165	-0.034	1	.854
4	OUT: TREERAT	467.204	-0.039	1	.843
5	OUT: MTDIST	467.233	-0.029	1	.864
6	OUT: LPOTR	467.277	-0.044	1	.833
7	OUT: LPIEN	469.709	-2.432	1	.119
8	OUT: MLDIST	469.789	-0.080	1	.777
9	OUT: MLDIAM	469.820	-0.031	1	.860
10	OUT: PCONCOV	470.692	-0.872	1	.350
11	OUT: PDECCOV	470.996	-0.304	1	.581
12	OUT: AVLITTER	471.330	-0.334	1	.563
13	OUT: DPOTR	471.663	-0.333	1	.564
14	OUT: PPOTRCV	472.030	-0.367	1	.545
15	OUT: CCAVE	472.543	-0.513	1	.474
16	OUT: MHFQ2	473.129	-0.586	1	.444
17	OUT: STEM2	473.631	-0.502	1	.479
18	OUT: LABLA	475.005	-1.374	1	.241
19	OUT: MSFQ2	476.500	-1.495	1	.222
20	OUT: GG	477.611	-1.111	1	.292

Backward selection model -2 Log Likelihood 514.414

Variable	B	S.E.	Wald	Sig
LOGAREA	14.6371	3.8470	14.4764	.0001
LOGRAT	2.8988	1.1306	6.5743	.0103
Constant	-2.0522	.1927	113.3926	.0000

Table G.19. Estimated habitat selection functions for Tamius minimus in the conifer habitat and south region built with logistic regression forward and backward selection routines in SPSS packages.

Forward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		82.462			
1	IN: MTDIST	77.423	5.039	1	.025
2	IN: LPIEN	70.769	6.654	1	.010
3	IN: LABLA	64.191	6.578	1	.010
4	OUT: MTDIST	66.220	-2.029	1	.154

Forward selection model -2 Log Likelihood 152.968

Variable	B	S.E.	Wald	Sig
MTDIST	.0021	.0015	1.8171	.1777
LPIEN	-51.9728	13.9440	13.8924	.0002
LABLA	-14.3906	5.8330	6.0865	.0136
Constant	-.6130	.8599	.5081	.4759

Backward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		40.970			
2	OUT: MSFQ3	40.971	-0.001	1	.980
3	OUT: LPOTR	40.972	-0.001	1	.980
4	OUT: POTHCOV	41.039	-0.067	1	.796
5	OUT: MHFQ2	41.041	-0.002	1	.965
6	OUT: GG	41.070	-0.029	1	.866
7	OUT: PCONCOV	41.141	-0.071	1	.790
8	OUT: TREERAT	41.215	-0.074	1	.786
9	OUT: MTDIAM	41.244	-0.029	1	.864
10	OUT: DPOTR	54.207	-12.963	1	.000
11	OUT: MTDIST	54.282	-0.075	1	.784
12	OUT: LOGAREA	54.439	-0.157	1	.692
13	OUT: AVLITTER	54.804	-0.365	1	.546
14	OUT: LOGRAT	55.400	-0.596	1	.440
15	OUT: MLDIAM	55.531	-0.131	1	.717
16	OUT: DPIEN	56.331	-0.800	1	.371
17	OUT: MHFQ3	57.173	-0.842	1	.359
18	OUT: MLDIST	57.781	-0.608	1	.435
19	OUT: GRFBS	59.023	-1.242	1	.265
20	OUT: DABLA	60.355	-1.332	1	.248
21	OUT: PDECCOV	62.482	-2.127	1	.145
22	OUT: STEM1	64.109	-1.627	1	.202

Backward selection model -2 Log Likelihood 154.773

Variable	B	S.E.	Wald	Sig
LABLA	-14.8121	5.6963	6.7616	.0093
LPIEN	-53.5442	13.8314	14.9863	.0001
Constant	.3124	.5019	.3876	.5336

Table G.20. Estimated habitat selection functions for Tamius minimus in the mixed habitat and south region built with logistic regression forward and backward selection routines in SPSS packages.

Forward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		115.140			
1	IN: LOGRAT	109.015	6.125	1	.013
2	IN: MTDIAM	104.837	4.178	1	.041
3	IN: MSFQ2	102.420	2.417	1	.120

Forward selection model -2 Log Likelihood 102.419

Variable	B	S.E.	Wald	Sig
LOGRAT	7.1811	2.9926	5.7581	.0164
MTDIAM	.0624	.0288	4.7004	.0302
MSFQ2	2.5245	1.4708	2.9459	.0861
Constant	-4.3631	1.0431	17.4941	.0000

Backward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		71.344			
2	OUT: STEM2	71.344	0.000	1	.999
3	OUT: STEM3	72.137	-0.793	1	.373
4	OUT: LPOTR	72.138	-0.001	1	.975
5	OUT: DPIEN	73.981	-1.843	1	.175
6	OUT: POTHCOV	73.981	0.000	1	.992
7	OUT: PCONCOV	81.655	-7.674	1	.006
8	OUT: AVLITTER	81.729	-0.074	1	.785
9	OUT: MLDIAM	81.824	-0.095	1	.758
10	OUT: PPOTRCV	81.974	-0.150	1	.699
11	OUT: MSFQ3	82.188	-0.214	1	.643
12	OUT: MHFQ3	82.473	-0.285	1	.593
13	OUT: MTDIST	82.966	-0.493	1	.483
14	OUT: MHFQ2	83.419	-0.453	1	.501
15	OUT: TREERAT	84.174	-0.755	1	.385
16	OUT: LOGAREA	84.898	-0.724	1	.395
17	OUT: STEM1	85.349	-0.451	1	.502
18	OUT: LABLA	85.758	-0.409	1	.523

Backward selection model -2 Log Likelihood 94.347

Variable	B	S.E.	Wald	Sig
GRFBS	-.0344	.0157	4.8192	.0281
MSFQ2	4.6993	2.4682	3.6250	.0569
MTDIAM	.1130	.0371	9.3076	.0023
MLDIST	-.0043	.0016	7.0050	.0081
DPOTR	31.6761	14.1250	5.0290	.0249
Constant	-4.1956	1.3201	10.1018	.0015

Table G.21. Estimated habitat selection functions for Zapus princeps, pooled over habitat and region, built with logistic regression forward and backward selection routines in SPSS packages.

Forward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		271.649			
1	IN: LOGAREA	259.840	11.809	1	.001

Forward selection model -2 Log Likelihood 346.723

Variable	B	S.E.	Wald	Sig
LOGAREA	-21.6053	7.2273	8.9364	.0028
Constant	-3.3654	.2588	169.0858	.0000

Backward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		207.676			
2	OUT: STEM2	207.685	-0.009	1	.923
3	OUT: STEM4	207.705	-0.020	1	.889
4	OUT: DPIEN	207.705	0.000	1	.991
5	OUT: MSFQ3	207.707	-0.002	1	.963
6	OUT: POTHCOV	208.088	-0.381	1	.537
7	OUT: DPICO	208.089	-0.001	1	.976
8	OUT: MSFQ2	210.029	-1.940	1	.164
9	OUT: LOGRAT	210.042	-0.013	1	.909
10	OUT: LPICO	213.846	-3.804	1	.051
11	OUT: STEM3	213.885	-0.039	1	.843
12	OUT: MLDIAM	214.026	-0.141	1	.708
13	OUT: LPOTR	214.223	-0.197	1	.657
14	OUT: LPIEN	234.554	-20.331	1	.000
15	OUT: AVLITTER	234.556	-0.002	1	.965
16	OUT: GG	234.635	-0.079	1	.779
17	OUT: STEM1	234.776	-0.141	1	.707
18	OUT: GRFBS	234.985	-0.209	1	.648
19	OUT: PCONCOV	237.579	-2.594	1	.107
20	OUT: MHFQ3	237.716	-0.137	1	.711
21	OUT: TREERAT	238.340	-0.624	1	.430
22	OUT: MTDIST	238.793	-0.453	1	.501
23	OUT: MLDIST	239.558	-0.765	1	.382
24	OUT: DABLA	240.246	-0.688	1	.407
25	OUT: PPOTRCV	244.607	-4.361	1	.037
26	OUT: MHFQ2	245.265	-0.658	1	.417
27	OUT: PDECCOV	247.633	-2.368	1	.124
28	OUT: DPOTR	250.008	-2.375	1	.123
29	OUT: CCAVE	252.372	-2.364	1	.124
30	OUT: LABLA	257.201	-4.829	1	.028
31	IN: LPIEN	244.220	12.981	1	.000

Backward selection model -2 Log Likelihood 326.342

Variable	B	S.E.	Wald	Sig
LOGAREA	-18.4526	7.2539	6.4709	.0110
MTDIAM	.0816	.0243	11.2280	.0008
LPIEN	-125.915	60.6808	4.3058	.0380
Constant	-5.3941	.7297	54.6479	.0000

Table G.22. Estimated Habitat Selection Function models for Microtus longicaudus pooled over habitats and regions built with Logistic regression forward and backward selection routines in SPSS packages.

Forward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		477.441			
1	IN: STEM2	474.085	3.356	1	.067
2	IN: STEM1	464.169	9.916	1	.002
3	IN: MLDIST	454.993	9.176	1	.002
4	IN: PDECCOV	446.713	8.280	1	.004
5	IN: LPICO	433.629	13.084	1	.000

Forward selection model

Variable	B	S.E.	Wald	Sig
STEM1	-1.2132	.6180	3.8533	.0496
STEM2	3.9714	1.5712	6.3888	.0115
STEM3	.4977	.2743	3.2917	.0696
STEM4	-10.7018	667.3208	.0003	.9872
MLDIST	-.0014	.0007	4.5474	.0330
PDECCOV	-.0652	.0224	8.4561	.0036
LPICO	-676.092	1752.9895	.1487	.6997
Constant	-2.7632	.2860	93.3144	.0000

Backward selection steps

Step	Variable	-2 Log Likelihood	G	df	Sig
0		398.629			
2	OUT: STEM4	398.767	-0.138	1	.711
3	OUT: DPICO	398.768	-0.001	1	.971
4	OUT: AVLITTER	398.772	-0.004	1	.948
5	OUT: POTHCOV	399.515	-0.743	1	.389
6	OUT: LPOTR	399.530	-0.015	1	.904
7	OUT: STEM1	399.550	-0.020	1	.886
8	OUT: DPIEN	400.810	-1.260	1	.262
9	OUT: MTDIST	400.839	-0.029	1	.866
10	OUT: LOGRAT	400.889	-0.050	1	.823
11	OUT: TREERAT	400.927	-0.038	1	.845
12	OUT: DPOTR	400.988	-0.061	1	.805
13	OUT: MHFQ3	401.054	-0.066	1	.798
14	OUT: PPOTRCV	401.139	-0.085	1	.771
15	OUT: LPICO	415.723	-14.584	1	.000

Backward selection model

Variable	B	S.E.	Wald	Sig
PDECCOV	-.0770	.0260	8.7783	.0030
GG	.5869	.3797	2.3891	.1222
MHFQ2	-.1725	.0816	4.4713	.0345
MTDIAM	.0540	.0250	4.6547	.0310
MLDIST	-.0016	.0007	4.8693	.0273
STEM1	-.7394	1.1791	.3932	.5306
STEM2	4.4230	1.8373	5.7950	.0161
STEM3	.8053	.3203	6.3214	.0119
STEM4	-9.4619	393.4688	.0006	.9808
LABLA	-14.1908	10.7908	1.7294	.1885
LPIEN	-80.7897	46.2287	3.0541	.0805
LPICO	-413.369	1065.2569	.1506	.6980
Constant	-4.1449	.7877	27.6867	.0000

APPENDIX H. Logistic regression forward and backward variable selection steps.

Table H.1. Logistic regression forward and backward variable selection steps for Clethrionomys gapperi in the aspen habitat and north region.

Forward selection

Step	Variable	-2 Log Likelihood	G	df	Sig
0		635.618			
1	IN: AVLITTER	619.494	16.124	1	.000
2	IN: MLDIST	603.554	15.940	1	.000
3	IN: MLDIAM	599.154	4.400	1	.036

Backward selection

Step	Variable	-2 Log Likelihood	G	df	Sig
0		583.219			
2	OUT: PPOTRCV	583.219	0.000	1	.989
3	OUT: STEM4	583.233	-0.014	1	.905
4	OUT: MTDIST	583.240	-0.007	1	.935
5	OUT: LOGAREA	583.249	-0.009	1	.923
6	OUT: DPOTR	583.312	-0.063	1	.802
7	OUT: PCONCOV	583.373	-0.061	1	.805
8	OUT: GRFBS	583.512	-0.139	1	.709
9	OUT: POTHCOV	584.499	-0.987	1	.321
10	OUT: TREERAT	584.606	-0.107	1	.743
11	OUT: GG	584.759	-0.153	1	.696
12	OUT: MTDIAM	585.043	-0.284	1	.594
13	OUT: LOGRAT	585.897	-0.854	1	.355
14	OUT: MSFQ2	586.647	-0.750	1	.386
15	OUT: MHFQ2	586.974	-0.327	1	.568
16	OUT: LABLA	587.476	-0.502	1	.479
17	OUT: CCAVE	588.358	-0.882	1	.348
18	OUT: PDECCOV	589.735	-1.377	1	.241
19	OUT: MSFQ3	591.272	-1.537	1	.215
20	OUT: LPOTR	593.186	-1.914	1	.166
21	OUT: MHFQ3	596.034	-2.848	1	.091

Table H.2. Logistic regression forward and backward variable slection steps for Clethrionomys gapperi in the conifer habitat and north region.

Forward selection

Step	Variable	-2 Log Likelihood	G	df	Sig
0		224.289			
1	IN: LOGAREA	214.865	9.424	1	.002
2	IN: PDECCOV	208.951	5.914	1	.015

Backward selection

Step	Variable	-2 Log Likelihood	G	df	Sig
0		183.622			
2	OUT: POTHCOV	183.626	-0.004	1	.948
3	OUT: LPICO	183.645	-0.019	1	.890
4	OUT: MSFQ3	183.665	-0.020	1	.888
5	OUT: MSFQ2	183.775	-0.110	1	.740
6	OUT: STEM1	184.139	-0.364	1	.547
7	OUT: MHFQ3	184.198	-0.059	1	.808
8	OUT: MTDIAM	184.295	-0.097	1	.756
9	OUT: MLDIST	184.419	-0.124	1	.725
10	OUT: PCONCOV	184.677	-0.258	1	.612
11	OUT: DPIEN	184.936	-0.259	1	.611
12	OUT: TREERAT	185.318	-0.382	1	.537
13	OUT: MHFQ2	185.739	-0.421	1	.517
14	OUT: LABLA	186.190	-0.451	1	.502
15	OUT: MLDIAM	187.099	-0.909	1	.340
16	OUT: AVLITTER	187.830	-0.731	1	.393
17	OUT: DABLA	188.999	-1.169	1	.280
18	OUT: LPIEN	190.513	-1.514	1	.219
19	OUT: GRFBS	191.625	-1.112	1	.292
20	OUT: PDECCOV	194.526	-2.901	1	.089
21	OUT: DPICO	196.246	-1.720	1	.190

Table H.3. Logistic regression forward and backward variable selection steps for Clethrionomys gapperi in the mixed habitat and north region.

Forward selection

Step	Variable	-2 LOG Likelihood	G	df	Sig
0		171.463			
1	IN: TREERAT	164.560	6.903	1	.009

Backward selection

Step	Variable	-2 Log Likelihood	G	df	Sig
0		137.722			
2	OUT: STEM1	137.722	0.000	1	.997
3	OUT: PPOTRCV	137.732	-0.010	1	.921
4	OUT: AVLITTER	137.746	-0.014	1	.905
5	OUT: MHFQ2	137.757	-0.011	1	.915
6	OUT: STEM3	137.934	-0.177	1	.674
7	OUT: LOGAREA	137.951	-0.017	1	.897
8	OUT: MSFQ2	140.131	-2.180	1	.140
9	OUT: LPICO	140.157	-0.026	1	.873
10	OUT: LPOTR	140.209	-0.052	1	.820
11	OUT: POTHCOV	141.160	-0.951	1	.329
12	OUT: MHFQ3	141.256	-0.096	1	.757
13	OUT: MSFQ3	141.355	-0.099	1	.753
14	OUT: LABLA	141.488	-0.133	1	.716
15	OUT: MTDIAM	141.821	-0.333	1	.564
16	OUT: DPICO	142.327	-0.506	1	.477
17	OUT: MLDIAM	142.936	-0.609	1	.435
18	OUT: DABLA	143.955	-1.019	1	.313
19	OUT: GG	144.678	-0.723	1	.395

Table H.4. Logistic regression forward and backward variable selection steps for Clethrionomys gapperi in the aspen habitat and south region.

Forward selection

Step	Variable	-2 Log Likelihood	G	df	Sig
0		555.656			
1	IN: STEM3	539.193	16.463	1	.000
2	IN: MHFQ2	526.692	12.501	1	.000
3	IN: MSFQ2	520.099	6.593	1	.010

Backward selection

Step	Variable	-2 Log Likelihood	G	df	Sig
0		488.253			
2	OUT: MTDIST	488.253	0.000	1	.994
3	OUT: STEM4	488.463	-0.210	1	.647
4	OUT: LOGAREA	488.478	-0.015	1	.903
5	OUT: STEM2	489.975	-1.497	1	.221
6	OUT: PCONCOV	492.000	-2.025	1	.155
7	OUT: LPIEN	492.109	-0.109	1	.741
8	OUT: GG	492.277	-0.168	1	.682
9	OUT: AVLITTER	492.588	-0.311	1	.577
10	OUT: MTDIAM	493.004	-0.416	1	.519
11	OUT: CCAVE	493.616	-0.612	1	.434
12	OUT: DPOTR	494.155	-0.539	1	.463
13	OUT: LPOTR	494.799	-0.644	1	.422
14	OUT: MHFQ3	496.009	-1.210	1	.271
15	OUT: PDECCOV	497.368	-1.359	1	.244
16	OUT: POTHCOV	498.553	-1.185	1	.276
17	OUT: TREERAT	500.022	-1.469	1	.225
18	OUT: PPOTRCV	503.241	-3.219	1	.073
19	OUT: MSFQ3	505.318	-2.077	1	.150
20	OUT: LABLA	508.368	-3.050	1	.081

Table H.5. Logistic regression forward and backward variable selection steps for Clethrionomys gapperi in the conifer habitat and south region.

Forward selection

Step	Variable	-2 Log Likelihood	G	df	Sig
0		141.332			
1	IN: MHFQ3	127.720	13.612	1	.000
2	IN: STEM1	119.273	8.447	1	.004

Backward selection

Step	Variable	-2 Log Likelihood	G	df	Sig
0		90.931			
2	OUT: MHFQ2	90.940	-0.009	1	.922
3	OUT: POTHCOV	91.158	-0.218	1	.640
4	OUT: MLDIAM	91.195	-0.037	1	.847
5	OUT: DPOTR	91.234	-0.039	1	.843
6	OUT: MSFQ3	94.092	-2.858	1	.091
7	OUT: MLDIST	94.241	-0.149	1	.699
8	OUT: LPIEN	94.438	-0.197	1	.657
9	OUT: CCAVE	94.879	-0.441	1	.506
10	OUT: AVLITTER	95.407	-0.528	1	.468
11	OUT: LPOTR	95.742	-0.335	1	.563
12	OUT: GRFBS	96.715	-0.973	1	.324
13	OUT: LOGRAT	98.358	-1.643	1	.200
14	OUT: LABLA	99.833	-1.475	1	.225
15	OUT: GG	100.922	-1.089	1	.297
16	OUT: LOGAREA	102.805	-1.883	1	.170
17	OUT: MTDIST	104.577	-1.772	1	.183
18	OUT: TREERAT	105.137	-0.560	1	.454
19	OUT: DABLA	107.534	-2.397	1	.122
20	OUT: MTDIAM	110.041	-2.507	1	.113
21	OUT: PDECCOV	112.251	-2.210	1	.137
22	OUT: DPIEN	115.601	-3.350	1	.067

Table H.6. Logistic regression forward and backward variable selection steps for Clethrionomys gapperi in the mixed habitat and south region.

Forward selection

Step	Variable	-2 Log Likelihood	G	df	Sig
0		179.497			
1	IN: LOGRAT	164.093	15.404	1	.000
2	IN : STEM3	157.681	6.412	1	.011

Backward selection

Step	Variable	-2 Log Likelihood	G	df	Sig
0		122.761			
2	OUT: MHFQ3	122.762	-0.001	1	.975
3	OUT: STEM1	122.768	-0.006	1	.937
4	OUT: PCONCOV	122.775	-0.007	1	.935
5	OUT: LOGRAT	122.783	-0.008	1	.928
6	OUT: STEM2	125.742	-2.959	1	.085
7	OUT: AVLITTER	125.742	0.000	1	.000
8	OUT: LPOTR	125.768	-0.026	1	.872
9	OUT: POTHCOV	127.247	-1.479	1	.224
10	OUT: DABLA	127.350	-0.103	1	.748
11	OUT: DPIEN	127.784	-0.434	1	.510
12	OUT: LOGAREA	128.284	-0.500	1	.480
13	OUT: DPOTR	128.707	-0.423	1	.516
14	OUT: CCAVE	129.376	-0.669	1	.414
15	OUT: MTDIAM	130.352	-0.976	1	.323
16	OUT: MSFQ3	132.451	-2.099	1	.147
17	OUT: PDECCOV	133.215	-0.764	1	.382
18	OUT: GG	134.206	-0.991	1	.320